

Result No.	Score	Query		DB	ID	Description
		Match	%			
1	634	80.9	144	5	Q9BJN0	Q9BJN0 boltenia vi
2	574.5	73.3	179	11	Q9D6E1	Q9D6E1 mus musculus
3	245.5	31.3	139	11	Q9CX13	Q9CX13 mus musculus
4	203.5	26.0	141	3	Q9PEK6	Q9PEK6 schizosacch
5	186.5	23.8	157	5	Q9VQL3	Q9VQL3 drosohila
6	170.5	21.7	137	10	Q8GMW5	Q8GMW5 arabidopsis
7	170	21.7	56	5	Q9SY55	Q9SY55 caenorhabdi
8	164.5	21.0	146	10	Q9C7D7	Q9C7D7 arabidopsis
9	163.5	20.9	166	10	Q9LH48	Q9LH48 arabidopsis
10	159.5	20.3	126	10	Q9LQ18	Q9LQ18 arabidopsis
11	141	18.0	92	4	Q9H0X8	Q9H0X8 homo sapien
12	139.5	17.8	455	10	Q9SLN31	Q9SLN31 arabidopsis
13	128	16.3	160	10	Q98RK9	Q98RK9 guillardia
14	122.5	15.6	110	10	Q9LNA7	Q9LNA7 arabidopsis
15	122.5	15.6	141	10	Q9SZ74	Q9SZ74 arabidopsis
16	90	11.5	249	3	Q9UTD3	Q9UTD3 schizosacch

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK01301; BAB22366.1; -
DR MGD; MGI:1925828; D53003D03RIK.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
SQ SEQUENCE 139 AA; 16089 MW; CA76B25D0D8EC091 CRC64;

Query Match 31.3%; Score 245.5; DB 11; Length 139;
Best Local Similarity 38.0%; Pred. No. 2.9e-18;
Matches 52; Conservative 24; Mismatches 60; Indels 1; Gaps 1;

QY 7 AFVYMLALLTAAALFFAIWHIIAFDELKTDYKPIDQCNLTNPLVPEYLLHFAFFCVMF 66
Db 3 AVWFESLDDCCALIFLSVFEIITLSLDECDYNARSCSKLNKWNIPELVGHITVTVLM 62
QY 67 LCAEWLTLGNMPLLAHYIWRYSRPMVSGPLGYDPTTINADILAYCQKGGCKLAFY 126
Db 63 LVSLHWFIFLLNPLVATWNIYRFIMVP-SGNMGVDFDTEIHRGQLKSHKMEAMIKLGFY 121
QY 127 LLAPFYLYGMIVYLVLS 143
Db 122 LLCFFWLYSMILALIN 138

RESULT 4
Q9P6K6 PRELIMINARY; PRT; 141 AA.
AC Q9P6K6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative er-derived vesicles protein similar to yeast erv14.
GN SPAC30C2.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL355652; CAB90792.1; -
DR GeneDB SPombe; SPAC30C2.05; -
DR InterPro; IPR003377; Cornichon.
DR D53003D03RIK.

Db 121 CKLAFLISFFYYLYRMIVLVLT 143
|||||:|||||:|||||:|||||:
121 CKLAFLISFFYYLYRMIVLVLT 143

RESULT 2
Q9D6E1 PRELIMINARY; PRT; 179 AA.
AC Q9D6E1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 2900075G08RIK.
GN 2900075G08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK013789; BAB28996.1; -
DR MGD; MGI:1920228; 2900075G08RIK.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
SQ SEQUENCE 179 AA; 21105 MW; B738709483743E82 CRC64;

Query Match 73.3%; Score 574.5; DB 11; Length 179;
Best Local Similarity 60.3%; Pred. No. 6.3e-53;
Matches 108; Conservative 13; Mismatches 23; Indels 35; Gaps 1;

QY 1 NAFTFAAFCYMLALLTAAALFFAIWHIIAFDELKTDYKPIDQCNLTN----- 49
Db 1 NAFTFAAFCYMLSLVLCALIFFAIWHIIAFDELKTDYKPIDQCNFPVHAFERLNERI 60
QY 50 -----PLVLPYLLHIAFFCMFLCAEWMFLGLNMLPLLAHY 85
Db 61 CFLLRKRVGPPGRRKRRGQQLVLPYSIHSFLCFMFLCAEWMFLGLNMLPLLYH 120
QY 86 IWRYSRPMVSGPLGYDPTTINADILAYCQKGGCKLAFVLLAPFYLYGMIVYLVSS 144
Db 121 FWRYPHCPADSELAYDPVPMNADTLGYCQKAWCKLAFVLLSFFYYLYCMIVTVLSS 179

RESULT 3
Q9CX13 PRELIMINARY; PRT; 139 AA.
AC Q9CX13;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE D53003D03RIK.
GN D53003D03RIK.

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DR Pfam; PF03311; Cornichon; 1.  
 DR PROSITE; PS01340; CORNICHON; 1.  
 SQ SEQUENCE 141 AA; 16614 MW; C9EBC2A6E89D1B5F CRC64;

Query Match 26.0%; Score 203.5; DB 3; Length 141;  
 Best Local Similarity 33.1%; Pred. No. 8.1e-14;  
 Matches 47; Conservative 25; Mismatches 55; Indels 15; Gaps 3;

OY 1 MAFTFAAFCYMLALLTAALIFPAIHIIAFDELKTDYKNPDIQCNTLNPLVLPYLPIHA 60  
 :|::||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|  
 12 LAVTF-----YRLGANMLLQICVMIFSDEMDYINPIDCNKLDNWPLISHT 63  
 :|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

OY 61 PFCMFCLAAEWLTGLNNPLLAYHWRMSRPMGPGLYDPTTIMNADILAYCQKEGW 120  
 :|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|  
 64 LVTLTLLGGKKWLLFLANLPLLVFH----ANQVIHKTHILDATETFR--LGRHKDNF 116  
 :|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

OY 121 CKLAFYLLAFFYYLYGMIVLV 142  
 :|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|  
 117 IKTVFLIMEFTLLYCWNLSLI 138  
 :|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 5  
 Q9VOL3 PRELIMINARY; PRT; 157 AA.

ID Q9VOL3 AC Q9VOL3  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE CG17262 protein.  
 GN CG17262

OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.P.,  
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Balow R.M., Basu A., Bavendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhattacharya D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Clayton S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
 RA Flesher C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murzyn D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,



```
SQ SEQUENCE 166 AA; 19478 MW; E4D7657A3F1FD77E CRC64;

Query Match      20.9%; Score 163.5; DB 10; Length 166;
Best Local Similarity 25.0%; Pred. No. 1.6e-09;
Matches 32; Conservative 32; Mismatches 57; Indels 7; Gaps 2;

Qy 8 FCYMLALLTAALIFFAIIHIIAFDELKTDYKPNIDOCNTLNPLVLPYLIHAFPCVMFL 67
Db 6 FLWIVSFVSVLWASVYQVICTDLEADYLNPNFETSTRNLRLVPIPEFILOGSLCLFL 65
Qy 68 CAAEWLTGLNMPLLAYHIWRMSPVMSGPGLYDPTTMMNADILAYCQKEGWCKLAFYL 127
Db 66 LTWHVFPVAVPVTVYHAMLYKERY-----LIDVTEVFRG--ISPEKRLRYKLGIVV 118
Qy 128 LAFYLYL 135
Db 119 FLFIWVVF 126

RESULT 10
Q9LQ18 ID Q9LQ18 PRELIMINARY; PRT; 126 AA.
AC Q9LQ18;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE F16P17.3 protein.
GN F16P17.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Sakano H., Liu S.X., Yu G., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA Chin C., Chioi J., Choi E., Chung M., Gonzalez A., Howng B., Liu A.,
RA Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
RA Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC F16P17 from Arabidopsis thaliana chromosome 1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011000; AAF75818.1; -.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon.
SQ SEQUENCE 126 AA; 15114 MW; CD61CBF896FC1827 CRC64;

Query Match      20.3%; Score 159.5; DB 10; Length 126;
Best Local Similarity 28.6%; Pred. No. 3.2e-09;
Matches 36; Conservative 29; Mismatches 54; Indels 7; Gaps 2;

Qy 10 YMLALLTAALIFFAIIHIIAFDELKTDYKPNIDOCNTLNPLVLPYLIHAFPCVMFLCA 69
Db 7 WIIISLITLGLVYLIADLEFDYINPYDSASRINFVLPESLQGLCVFLVLT 66
Qy 70 AEWLTGLNMPLLAYHIWRMSPVMSGPGLYDPTTMMNADILAYCQKEGWCKLAFYLLA 129
Db 67 GHWFVALLCVPLYNYNPLYSRK-----QHLIDVTEIFN--LLDWEKKRLFLAYIILT 119
Qy 130 FFYLYL 135
Db 120 LFLTIF 125

RESULT 11
Q9H0X8 ID Q9H0X8 PRELIMINARY; PRT; 92 AA.
AC Q9H0X8;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 22, Last annotation update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
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DE Hypothetical protein.
GN DKFZP586E122.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=21154917; PubMed=11230166;
RA Wisemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansong W., Boecher M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.W., Ottenwaelder B., Obermaier B., Rampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
RL Genome Res. 11:422-435(2001).
DR EMBL; AL136930; CAB66864.1; -.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon.
KW Hypothetical protein.
SQ SEQUENCE 92 AA; 10615 MW; A99857E36401B352 CRC64;

Query Match      18.0%; Score 141; DB 4; Length 92;
Best Local Similarity 34.1%; Pred. No. 2.1e-07;
Matches 28; Conservative 18; Mismatches 36; Indels 0; Gaps 0;

Qy 7 AFCYMLALLTAALIFFAIIHIIAFDELKTDYKPNIDOCNTLNPLVLPYLIHAFPCVMF 66
Db 3 AVVFSLLDCCALIFLSVFIITLSDECDYINARSCCKLNKWKVPELIGHITVTVLL 62
Qy 67 LCAAEWLTGLNMPLLAYHIWR 88
Db 63 LMSLHWFFTLNLPVATWNIYR 84

RESULT 12
Q9LNB1 ID Q9LNB1 PRELIMINARY; PRT; 455 AA.
AC Q9LNB1;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE F5011.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chioi J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F5011 from chromosome
RT I.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
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RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC025416; AAF79631.1; -.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
SQ SEQUENCE 455 AA; 51561 MW; D6CE7BD380BAF0C CRC64;

Query Match      17.8%; Score 139.5; DB 10; Length 455;
Best Local Similarity 33.3%; Pred. No. 1.5e-06;
Matches 28; Conservative 14; Mismatches 37; Indels 5; Gaps 1;

QY 25 IWHITAFDELKTDYKNPIDQCNLTNPLVPEYLHAFPCVMEFLCAAEWLTGLNNPLLAY 84
Db 14 IFHLVCLADLEFDYINPYDSASRINSVLPPEFVQVLCVFLYLLTGHFWMTLLCLPLYLY 73

QY 85 HIWRYMRPVMSPGGLYDPTIMN 108
Db 74 NFHLYSKR-----QHLVDVTEIFN 92

RESULT 13
Q98RK9 PRELIMINARY; PRT; 160 AA.
AC Q98RK9;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 18.7 kDa protein orf160 from chromosome 1 (Hypothetical
DE 18.7 kDa protein orf160 from chromosome 3).
GN ORF160.
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
QX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21223349; PubMed=11233671;
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
RA Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
RT "The highly reduced genome of an enslaved algal nucleus.";
RL Nature 410:1091-1096(2001).
DR EMBL; AF165818; AAK39902.1; -.
DR EMBL; AF083031; AAK39731.1; -.
DR EMBL; AF083031; AAK39781.1; -.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
KW Hypothetical protein.
SQ SEQUENCE 160 AA; 18743 MW; 56BEDEF0230C7B15 CRC64;

Query Match      16.3%; Score 128; DB 10; Length 160;
Best Local Similarity 29.4%; Pred. No. 8.7e-06;
Matches 32; Conservative 22; Mismatches 47; Indels 8; Gaps 3;

QY 33 ELKTDYKNPIDQCNLTNPLVPEYLHAFPCVMEFLCAAEWLTGLNNPLLAYHIWYMSR 92
Db 38 DLSTDTNVEVCDKQVKPEYLAHLFLSLAFVIRGWWIVGFLNPFPIFYNAQW--- 94

QY 93 PVMSPGGLYDPTIMNADILAYCQEGWCKLAFYLLAFYLY-GMIYV 140
Db 95 --YEGHQHLSAQIFN--VLSRELRIKAKSAFFIIIVITWENMIW 139

RESULT 14
Q9LNA7 PRELIMINARY; PRT; 110 AA.
AC Q9LNA7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

```

```

DE F5011.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F5011 from chromosome
RT 1.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC025416; AAF79633.1; -.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
SQ SEQUENCE 110 AA; 13003 MW; 8C6D066C5DDCC67D CRC64;

Query Match      15.6%; Score 122.5; DB 10; Length 110;
Best Local Similarity 25.4%; Pred. No. 2.3e-05;
Matches 32; Conservative 26; Mismatches 45; Indels 23; Gaps 4;

QY 10 YMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLHAFPCVMEFLCA 69
Db 7 WLISFFFIALVGIIVQVCLADLEFDYINPYDSASRINSVLPPEFVQVLCVY--- 63

QY 70 AEWLTGLNMPLLAYHIWYMSRPMVSPGGLYDPTIMNADILAYCQEGWCKLAFYLLA 129
Db 64 -----LLTCHC--YSKR-----QHLVDVTEIFN--LLNWEKKRFLKAYIVLN 103

QY 130 PFYLY 135
Db 104 LFLTIF 109

RESULT 15
Q9SZ74 PRELIMINARY; PRT; 145 AA.
AC Q9SZ74;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 17.3 kDa protein.
GN F16J13.160 OR AT4G12090.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

```

Search completed: September 11, 2003, 14:39:55  
Job time : 109 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:36:35 ; Search time 23 Seconds  
(without alignments)  
294.428 Million cell updates/sec

Title: US-09-918-585A-322

Perfect score: 784

Sequence: 1 MAFTFAAFYLYGMIVLVSS 144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	784	100.0	144	1	CNIH_HUMAN
2	778	99.2	144	1	CNIH_MOUSE
3	586	74.7	160	1	CNIH_HUMAN
4	575	73.3	160	1	CNIH_MOUSE
5	548	69.9	144	1	CNI_DROME
6	544	65.4	144	1	CNI_DROVI
7	472	60.2	145	1	YFR3_CABEL
8	244.5	31.2	139	1	H163_HUMAN
9	212.5	27.1	137	1	ERV4_YEAST
10	204.5	26.1	134	1	YEV5_SCHPO
11	193.5	24.7	142	1	YB60_YEAST
12	84.5	10.8	256	1	TATC_HAEIN
13	82.5	10.5	802	1	YGN9_YEAST
14	81	10.3	446	1	NU4M_CERCA
15	79.5	10.1	621	1	P212_MOUSE
16	78.5	10.0	305	1	T2RD_RAT
17	77.5	9.9	296	1	YESQ_BACSU
18	75.5	9.6	209	1	Y1L3_YEAST
19	74.5	9.5	458	1	SSU1_YEAST
20	74	9.4	253	1	YDIJ_BACHD
21	73	9.3	258	1	TATC_SCOLI
22	73	9.3	363	1	CYB_TRYBB
23	72.5	9.2	256	1	YM56_YEAST
24	72.5	9.2	385	1	CYB_ACACA
25	72	9.2	381	1	CYB_NEOAL
26	72	9.2	797	1	S6A5_HUMAN
27	72	9.2	799	1	S6A5_RAT
28	71	9.1	171	1	YB74_YEAST
29	71	9.1	441	1	DIHR_ACHDO
30	71	9.1	459	1	NU4M_BOVIN
31	71	9.1	558	1	AGP3_YEAST
32	70.5	9.0	401	1	NH65_CABEL
33	70	8.9	400	1	T2R9_MOUSE

34 70 8.9 390 1 O85B\_DROME  
35 70 8.9 852 1 WS14\_HUMAN  
36 70 8.9 2039 1 CCH1\_YEAST  
37 69.5 8.9 307 1 T2RA\_HUMAN  
38 69.5 8.9 372 1 CYB\_TRYBO  
39 69.5 8.9 395 1 DIHR\_MANSE  
40 69 8.8 369 1 Y116\_MYCPN  
41 69 8.8 557 1 OM6\_CHLPS  
42 68.5 8.7 363 1 YRU5\_CAEEL  
43 68 8.7 395 1 YN84\_CAEEL  
44 68 8.7 435 1 EXOQ\_RHIME  
45 67.5 8.6 208 1 H1S1\_THEME

#### ALIGNMENTS

RESULT 1  
CNIH\_HUMAN  
ID CNIH\_HUMAN STANDARD; PRT; 144 AA.  
AC O95406;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cornichon homolog (IGAM77).  
GN CNIH OR CNIL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Carcinoma;  
RA Plisov S.Y., Ivanov S.V., Lerman M., Perantoni A.O.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=20499367; PubMed=11042152;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
300 previously undefined genes expressed in CD34+ hematopoietic  
stem/progenitor cells.";  
RL Genome Res. 10:1546-1560(2000).  
RN [3]  
RP SEQUENCE OF 11-144 FROM N.A.  
RX MEDLINE=99227056; PubMed=10209299;  
RA Utoku N., Bulwin G.-C., Beinke S., Heinemann T., Beato F., Randall J.,  
Schneiders B., Sandhoff K., Volk H.-D., Milford E., Gullans S.R.;  
RT "The human homolog of Drosophila cornichon protein is differentially  
expressed in alloactivated T-cells.";  
RL Biochim. Biophys. Acta 1449:203-210(1999).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LIVER, SKELETAL  
MUSCLE, PANCREAS, ADRENAL MEDULLA AND CORTEX, THYROID, TESTIS,  
SPLEEN, APPENDIX, PERIPHERAL BLOOD LYMPHOCYTES AND BONE MARROW.  
CC LOWER EXPRESSION FOUND IN BRAIN, PLACENTA, LUNG, KIDNEY, OVARY,  
SMALL INTESTINE, STOMACH, LYMPH NODE, THYMUS AND FETAL LIVER.  
CC -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; AF104398; AAC38388.1; -;  
CC EMBL; AF070654; AAD20960.1; -;  
CC EMBL; AF031379; AAD32301.1; -;

DR Genew; HGNC:19431; CNH.  
DR GO; GO:0006955; P:immune response; TAS.  
DR InterPro; IPR003377; Cornichon.  
DR Pfam; PF03311; Cornichon; 1.  
DR PROSITE; PS01340; CORNICHON; 1.  
KW Transmembrane.  
FT TRANSMEM 11 31 POTENTIAL.  
FT TRANSMEM 57 77 POTENTIAL.  
FT TRANSMEM 123 143 POTENTIAL.  
SQ SEQUENCE 144 AA; 16699 MW; 59BD114D24C455CD CRC64;  
  
Query Match 100.0%; Score 784; DB 1; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1.5e-68; Indels 0; Gaps 0;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAFTFAFCVMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVPEYLIHA 60  
DB 1 MAFTFAFCVMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVPEYLIHA 60  
  
QY 61 FFCVWFLCAAEWLTGLNPLLAYHIWYMSRPMVSGGLYDPTTINMADILAYCQKEGW 120  
DB 61 FFCVWFLCAAEWLTGLNPLLAYHIWYMSRPMVSGGLYDPTTINMADILAYCQKEGW 120  
  
QY 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
DB 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
  
RESULT 2  
ID CNH\_MOUSE STANDARD; PRT; 144 AA.  
AC O35372;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cornichon homolog.  
GN CNH...  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=B6D2;  
RX MEDLINE=99147138; PubMed=10022955;  
RA Hwang S.-Y., Oh B., Zhang Z., Miller W., Solter D., Knowles B.B.;  
RT "The mouse cornichon gene family."  
RL Dev. Genes Evol. 209:120-125(1999).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN OOCYTES, AND AT A BASAL LEVEL IN OVARIAN SOMATIC CELLS OF 6-WEEK-OLD MOUSE. EXPRESSED IN ADULT BRAIN.  
CC -1- DEVELOPMENTAL STAGE: ABUNDANT IN FULL GROWN OOCYTE AND THE OVULATED UNFERTILIZED EGG, SHOWS A SLIGHT DECREASE 12 HOURS AFTER FERTILIZATION. TRANSCRIPTS FROM THE ACTIVATED EMBRYONIC GENOME ARE PRESENT IN THE EIGHT-CELL EMBRYO.  
CC -1- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.  
-----  
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-----  
EMBL; AF022811; AAC15828.1; ..  
DR MGD; MGI:1277202; Cnih.  
DR InterPro; IPR003377; Cornichon.  
DR Pfam; PF03311; Cornichon; 1.  
DR PROSITE; PS01340; CORNICHON; 1.  
KW Transmembrane.  
FT TRANSMEM 11 31 POTENTIAL.

FT TRANSMEM 57 77 POTENTIAL.  
FT TRANSMEM 123 143 POTENTIAL.  
SQ SEQUENCE 144 AA; 16713 MW; DF66786D24C455CA CRC64;  
  
Query Match 99.2%; Score 778; DB 1; Length 144;  
Best Local Similarity 99.3%; Pred. No. 5.7e-68; Indels 1; Gaps 0;  
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MAFTFAFCVMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVPEYLIHA 60  
DB 1 MAFTFAFCVMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVPEYLIHA 60  
  
QY 61 FFCVWFLCAAEWLTGLNPLLAYHIWYMSRPMVSGGLYDPTTINMADILAYCQKEGW 120  
DB 61 FFCVWFLCAAEWLTGLNPLLAYHIWYMSRPMVSGGLYDPTTINMADILAYCQKEGW 120  
  
QY 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
DB 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
  
RESULT 3  
ID CNIL\_HUMAN STANDARD; PRT; 160 AA.  
AC Q8TBE1;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Cornichon-like protein.  
GN CNIL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;  
RT "NEO human cDNA sequencing project";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.F., Casavant T.L., Schetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.  
-----  
CC

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DR EMBL; AK096312; BAC04760.1; -;  
 DR EMBL; BC022780; AA022780.1; -;  
 DR InterPro; IPR003377; Cornichon.  
 DR Pfam; PF03311; Cornichon; 1.  
 DR PROSITE; PS01340; CORNICHON; FALSE\_NEG.  
 KW Transmembrane.  
 FT TRANSMEM 11 31 POTENTIAL.  
 FT TRANSMEM 73 93 POTENTIAL.  
 FT TRANSMEM 139 159 POTENTIAL.  
 SQ SEQUENCE 160 AA; 18976 MW; CPT7E8645A9587504 CRC64;

Query Match 74.7%; Score 586; DB 1; Length 160;  
 Best Local Similarity 68.1%; Pred. No. 1.7e-49;  
 Matches 109; Conservative 11; Mismatches 24; Indels 16; Gaps 1;

OY 1 MAFTFAAFYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCN----- 46  
 DB 1 MAFTFAAFYMLSLVLCALFFAIWHIIAFDELKSPIDQCNFVHARERLNRIERI 60  
 OY 47 --TLNPLVLYLHAFPCVMFLCAEWLTLGLNMLLAYHIWRYMSPVMSGGLYDPT 104  
 DB 61 CFLRLKLVLPYSIHSFLCFMFLCAEWLTLGLNPLVLYLHAFPCVMSGLAYDPP 120  
 OY 105 TIMNADILAYCQKEGWCKLAFYLLAFYLYGMIVLVSS 144  
 DB 121 VVMDATLSYCKEAWCKLAFYLLSFFYLYCMIVLVSS 160

## RESULT 4

ID CNIL\_MOUSE STANDARD; PRT; 160 AA.  
 AC O35089;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cornichon-like protein.  
 GN CNIL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Fetal brain;  
 RA Fujimoto N., Kawamoto S., Matsubara K., Okubo K.;  
 RT "Cloning of mouse homologue of Drosophila cornichon protein from 17.5  
 RL dpc fetal brain";  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.  
 RX MEDLINE=9147138; PubMed=10022955;  
 RA Hwang S.-Y., Oh B., Zhang Z., Miller W., Solter D., Knowles B.B.;  
 RT "The mouse cornichon gene family";  
 RL Dev. Genes Evol. 209:120-125(1999).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN EIGHT-CELL EMBRYO, BLASTOCYST,  
 CC 6.5-DAY WHOLE EMBRYO, 7.5-DAY PRIMITIVE STREAK, 11.5-DAY LIMB BUD  
 CC AND IN 13.5-DAY WHOLE EMBRYO. ALSO IN ADULT LUNG AND BRAIN.  
 CC -!- DEVELOPMENTAL STAGE: First detected at the eight-cell stage.  
 CC -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.

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DR EMBL; AB006191; BAA21746.2; -;  
 DR MGD; MGI:1277225; Cnrl.  
 DR InterPro; IPR003377; Cornichon.  
 DR Pfam; PF03311; Cornichon; 1.  
 DR PROSITE; PS01340; CORNICHON; 1.  
 KW Transmembrane.  
 FT TRANSMEM 11 31 POTENTIAL.  
 FT TRANSMEM 73 93 POTENTIAL.  
 FT TRANSMEM 139 159 POTENTIAL.  
 SQ SEQUENCE 160 AA; 18931 MW; 00330E5E609B28BF CRC64;

Query Match 73.3%; Score 575; DB 1; Length 160;  
 Best Local Similarity 66.0%; Pred. No. 1.9e-48;  
 Matches 105; Conservative 13; Mismatches 25; Indels 16; Gaps 1;

OY 1 MAFTFAAFYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQ----- 44  
 DB 1 MAFTFAAFYMLTLVLCASLFFVWHIIAFDELKTDKPNIDQGNPARARERLNRIERI 60  
 OY 45 CNTNPLVLYLHAFPCVMFLCAEWLTLGLNMLLAYHIWRYMSPVMSGGLYDPT 104  
 DB 61 CCLRLKLVLPYSIHSFLCFMFLCAEWLTLGLNPLVLYLHAFPCVMSGLAYDPP 120  
 OY 105 TIMNADILAYCQKEGWCKLAFYLLAFYLYGMIVLVSS 143  
 DB 121 SIMNADILAYCQKEGWCKLAFYLLSFFYLYSMVTLVS 159

## RESULT 5

ID CNIL\_DROME STANDARD; PRT; 144 AA.  
 AC P49858; Q9V423;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cornichon protein.  
 GN CNIL OR CG5855.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=95300228; PubMed=7540118;  
 RA Roth S., Neuman-Silberberg F.S., Barcelo G., Schuepbach T.;  
 RT "Cornichon and the EGF receptor signaling process are necessary for  
 RT both anterior-posterior and dorsal-ventral pattern formation in  
 RT Drosophila";  
 RL Cell 81:967-978(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=99403001; PubMed=10471707;  
 RA Ashburner M., Misra S., Rote J., Lewis S.E., Blazej R.G., Davis T.,  
 RA Doyle C., Galle R.F., George R.A., Harris N.L., Hartzell G.,  
 RA Harvey D., Hong L., Houston K.A., Hoskins R.A., Johnson G., Martin C.,  
 RA Moshrefi A., Palazzolo M., Reese M.G., Spradling A.C., Teang G.,  
 RA Wan K.H., Whitelaw K., Celnik S.E., Rubin G.M.;  
 RT "An exploration of the sequence of a 2.9-Mb region of the genome of  
 RT Drosophila melanogaster: the Adh region";  
 RL Genetics 153:179-219(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazew R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de la Bazo J., Delcher A., Dew Z., Dwan R., Dwan S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stappleton M., Strong R., Sun E., Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).

CC -1- FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY TORPEDO RESULTING IN A SIGNALING PATHWAY THAT FIRST ESTABLISHES POSTERIOR FOLLICLE CELL FATES AND NORMAL LOCALIZATION OF THE ANTERIOR AND POSTERIOR DETERMINANTS, LATER THEY ACT IN A SIGNALING EVENT INDUCING DORSAL FOLLICLE CELL FATES AND REGULATING THE DORSAL-VENTRAL PATTERN OF EGG AND EMBRYO.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- DEVELOPMENTAL STAGE: IN EARLY STAGES. IT IS PRESENT IN THE NURSE CELL OOCYTE CLUSTER. IT IS HIGHLY EXPRESSED IN STAGE 1-6 EGG CHAMBERS, EXPRESSION CEASES DURING STAGE 7 AND CANNOT BE DETECTED IN STAGES 8 AND 9. DURING STAGE 10, IT IS REEXPRESSED IN THE NURSE CELLS.

CC -1- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.

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CC EMBL; U28069; A56724; -  
CC EMBL; AE003415; AAF45003.1; -  
CC DR EMBL; AE003650; AAF53521.1; -  
CC PIR; A56724; A56724.  
CC DR FlyBase; FBgn0000339; cni.  
CC InterPro; IPR003377; Cornichon.  
CC Pfam; PF03311; Cornichon; 1.  
CC PROSITE; PS01340; CORNICHON; 1.  
CC Developmental protein; Transmembrane.  
CC TRANSMEM 11 31 POTENTIAL.  
CC TRANSMEM 57 77 POTENTIAL.  
CC TRANSMEM 123 143 POTENTIAL.  
CC SEQUENCE 144 AA; 16931 MW; 27692A3F68ECE1A9 CRC64;

Query Match 69.9%; Score 548; DB 1; Length 144;  
Best Local Similarity 66.7%; Pred. No. 1.7e-45;  
Matches 96; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 MAFTFAFCYMLALLTLTAALIFFAIWHIAFDLKTQYKNPIDQCNTLNPLVPEYLIIHA 60  
DB 1 MAFNFTAFYIVALLIGDAFLIFFAIWHIAFDLKTQYKNPIDQCNTLNPLVPEYLIIHA 60  
QY 61 FFCWMLCAAEWLTGLNPLLAYHYWYMSRPMVSGPLGYDPTTIMNADILAYCOKEGW 120  
DB 61 FLNLLFLFCGEWFSCLNPLIAYHIWYKRNPLMSGPGLYDPTTVLKTDTLFRNLREGW 120  
QY 121 CKLAFYLLAFYFYLYGMIVLVSS 144  
DB 121 IKLAVYLISFFYYIYGMVYSLIST 144

RESULT 6  
CNI\_DROVI STANDARD; PRT; 144 AA.  
AC PS3159;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cornichon protein.  
GN CNI.  
OS Drosophila virilis (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7244;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=95300228; PubMed=7540118;  
RA Roth S., Neuman-Silberberg F.S., Barcelo G., Schuepbach T.;  
RT "Cornichon and the EGF receptor signaling process are necessary for both anterior-posterior and dorsal-ventral pattern formation in Drosophila";  
RL Cell 81:967-978(1995).

CC -1- FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY TORPEDO RESULTING IN A SIGNALING PATHWAY THAT FIRST ESTABLISHES POSTERIOR FOLLICLE CELL FATES AND NORMAL LOCALIZATION OF THE ANTERIOR AND POSTERIOR DETERMINANTS, LATER THEY ACT IN A SIGNALING EVENT INDUCING DORSAL FOLLICLE CELL FATES AND REGULATING THE DORSAL-VENTRAL PATTERN OF EGG AND EMBRYO (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.

CC FlyBase; FBgn0015209; Dvir\cni.  
CC InterPro; IPR003377; Cornichon.  
CC Pfam; PF03311; Cornichon; 1.  
CC PROSITE; PS01340; CORNICHON; 1.  
CC Developmental protein; Transmembrane.  
CC TRANSMEM 11 31 POTENTIAL.  
CC TRANSMEM 57 77 POTENTIAL.  
CC TRANSMEM 123 143 POTENTIAL.  
CC SEQUENCE 144 AA; 16927 MW; D0F4E5560409164 CRC64;

Query Match 69.4%; Score 544; DB 1; Length 144;  
Best Local Similarity 66.7%; Pred. No. 1.7e-45;  
Matches 96; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 MAFTFAFCYMLALLTLTAALIFFAIWHIAFDLKTQYKNPIDQCNTLNPLVPEYLIIHA 60  
DB 1 MAFNFTAFYIVALLIGDAFLIFFAIWHIAFDLKTQYKNPIDQCNTLNPLVPEYLIIHA 60  
QY 61 FFCWMLCAAEWLTGLNPLLAYHYWYMSRPMVSGPLGYDPTTIMNADILAYCOKEGW 120  
DB 61 FLNLLFLFCGEWFSCLNPLIAYHIWYKRNPLMSGPGLYDPTTVLKTDTLFRNLREGW 120  
QY 121 CKLAFYLLAFYFYLYGMIVLVSS 144  
DB 121 IKLAVYLISFFYYIYGMVYSLIST 144

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazew R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de la Bazo J., Delcher A., Dew Z., Dwan R., Dwan S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stappleton M., Strong R., Sun E., Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).

CC -1- FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY TORPEDO RESULTING IN A SIGNALING PATHWAY THAT FIRST ESTABLISHES POSTERIOR FOLLICLE CELL FATES AND NORMAL LOCALIZATION OF THE ANTERIOR AND POSTERIOR DETERMINANTS, LATER THEY ACT IN A SIGNALING EVENT INDUCING DORSAL FOLLICLE CELL FATES AND REGULATING THE DORSAL-VENTRAL PATTERN OF EGG AND EMBRYO.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- DEVELOPMENTAL STAGE: IN EARLY STAGES. IT IS PRESENT IN THE NURSE CELL OOCYTE CLUSTER. IT IS HIGHLY EXPRESSED IN STAGE 1-6 EGG CHAMBERS, EXPRESSION CEASES DURING STAGE 7 AND CANNOT BE DETECTED IN STAGES 8 AND 9. DURING STAGE 10, IT IS REEXPRESSED IN THE NURSE CELLS.

CC -1- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.

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CC EMBL; U28069; A56724; -  
CC EMBL; AE003415; AAF45003.1; -  
CC DR EMBL; AE003650; AAF53521.1; -  
CC PIR; A56724; A56724.  
CC DR FlyBase; FBgn0000339; cni.  
CC InterPro; IPR003377; Cornichon.  
CC Pfam; PF03311; Cornichon; 1.  
CC PROSITE; PS01340; CORNICHON; 1.  
CC Developmental protein; Transmembrane.  
CC TRANSMEM 11 31 POTENTIAL.  
CC TRANSMEM 57 77 POTENTIAL.  
CC TRANSMEM 123 143 POTENTIAL.  
CC SEQUENCE 144 AA; 16931 MW; 27692A3F68ECE1A9 CRC64;

Query Match 69.9%; Score 548; DB 1; Length 144;

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RESULT 7
YFR3_CAEEL
ID YFR3_CAEEL STANDARD; PRT; 145 AA.
AC Q22361;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 16.8 kDa protein T09E8.3 in chromosome V.
GN T09E8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Steward C.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Durbin R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z78065; CAB01516.2; -.
DR PIR; T24750; T24750.
DR WormPep; T09E8.3; CE23961.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
DR PROSITE; PS01340; CORNICHON; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 5 25 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
SQ SEQUENCE 145 AA; 16830 MW; 5C1C032B25DCE73C CRC64;
Query Match 60.2%; Score 472; DB 1; Length 145;
Best Local Similarity 59.0%; Pred. No. 1.4e-38;
Matches 85; Conservative 24; Mismatches 35; Indels 0; Gaps 0;
Qy 1 MAFTFAFCYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLIHA 60
Db 1 MAFTFAFCYLLALIAVGFCIFFAIYVICVDELRTDYKNPIEQCRNLNQLILPEYIIG 60
Qy 61 PFCVWFLCAEWLTLGLNPLLAYHIWYMRPVMGSGGLYDPTTINMADILAYCQKGGW 120
Db 61 TFTVLTFPSWGLISILANLPLAFYHIYTYAKRPVMSGPGIYDPTTLNRLSTLSLISW 120
Qy 121 CKLAFYLAFYYLYGMYYLVSS 144
Db 121 IKLAFYLVSFYYLYAMYYTLVTS 144
RESULT 8
H163_HUMAN
ID H163_HUMAN STANDARD; PRT; 139 AA.
AC Q9P003;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein HSPC163.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20499167; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells."
RL Genome Res. 10:1546-1560(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC -----
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CC -----
DR EMBL; AF161512; AAF29127.1; -.
DR EMBL; BC000573; AAH00573.1; -.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
KW Transmembrane.
FT TRANSMEM 5 25 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 118 138 POTENTIAL.
SQ SEQUENCE 139 AA; 16093 MW; 9452E9BDEC2A8DEF CRC64;
Query Match 31.2%; Score 244.5; DB 1; Length 139;
Best Local Similarity 38.0%; Pred. No. 9e-17;
Matches 52; Conservative 24; Mismatches 60; Indels 1; Gaps 1;
Qy 7 AFCYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLIHAFYCYVMF 66
Db 3 AVFVFSLLDCCALIFLSVFIITLSDLECDYINARSCCKLNKWKVPELIGHITVTVLL 62
Qy 67 LCAAEWLTLGLNPLLAYHIWYMRPVMGSGGLYDPTTINMADILAYCQKGGWCKLAFY 126
Db 63 LMSLHWEIFLNLPLVATWNIYRIYIMVP-SGNMGVFDPTTEIHNRGQLKSHMKEAMIKLGFH 121
Qy 127 LLAFFYLYGMYYLVSS 143
Db 122 LLCFFMYLYSMILALIN 138

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Best Local Similarity 32.8%; Pred. No. 1.1e-13;  
Matches 45; Conservative 31; Mismatches 54; Indels 7; Gaps 2;

QY 7 AFYMLALLTAAALFFFAIWHIIAFDELKTDYKNIPDOCNTPNPLVLYLHAFECYMF 66  
DB 2 AWLFILAVVVCINLFGQVHFTILYADLEADYINPIELCKVKNLITPEALHGLSLLF 61  
QY 67 LCAAEWLTGLNWPPLLYHWRMSRPMVSGPLGVDPTIMNADILAYCOKEGWCKLAFY 126  
DB 62 LLNGYWFVFLNLPVLYNL-----NKIYKVLQDLDATEIFPT--LGKHKRSFLKLGPH 114  
QY 127 LLAFFVYLYGMIYVLVS 143  
DB 115 LLNFFVLYRMIMALIA.131

RESULT 10

YEVS SCHPO

ID YEVS SCHPO STANDARD; PRT; 134 AA.

AC 014038;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical protein C2C4.05 in chromosome I.

GN SPAC2C4.05.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OC NCBI\_TaxID=4896;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RC MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgrooks J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown N., Brown S., Chillingworth T., Church C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Welljens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Lucas M., Rochet M., Gaillardin C., Talla V.A., Garzon A., Thode G.,

RA Paga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerretti L., Lowe I., Ussery D., Barrell B.G., Nurse P.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

RT "The genome sequence of Schizosaccharomyces pombe."

RL Nature 415:871-880(2002).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- SIMILARITY: BELONGS TO THE CORNICION FAMILY.

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CC -----

CC EMBL; Z99259; CAB16365.1; -

CC PIR; T38516; T38516.

DR

RESULT 9  
ID ERV4 YEAST STANDARD; PRT; 137 AA.  
AC P53173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE ER-derived vesicles protein ERV14.  
GN ERV14 OR YGL054C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OC NCBI\_TaxID=4932;  
RP [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=9737793; PubMed=9234674;  
RC MEDLINE=9237793; PubMed=9234674;  
RA Feuerhahn M., de Montigny J., Potier S., Souciet J.-L.;  
RT "The characterization of two new clusters of duplicated genes  
RT suggests a 'lego' organization of the yeast Saccharomyces cerevisiae  
RT chromosomes.";  
RL Yeast 13:861-869(1997).  
RP [2]

RP SEQUENCE OF 1-18, AND FUNCTION.  
RX MEDLINE=98402530; PubMed=9732282;  
RA Powers J., Barlowe C.;  
RT "Transport of axl2p depends on erv14p, an ER-vesicle protein related  
RT to the Drosophila cornichon gene product.";  
RL J. Cell Biol. 142:1209-1222(1998).  
CC -1- FUNCTION: COULD REGULATE EXPORT OF THE BUD SITE AND AXIAL GROWTH  
CC SITES SELECTION PROTEIN AXL2 AND POSSIBLY OTHER SECRETORY  
CC PROTEINS FROM THE ENDOPLASMIC RETICULUM IN COPII-COATED VESICLES.  
CC SEEMS TO BE REQUIRED FOR AXIAL BUDDING PATTERN IN HAPLOID CELLS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. RESIDES IN THE  
CC ENDOPLASMIC AND GOLGI COMPARTMENTS, AND THEN PACKAGED INTO  
CC ENDOPLASMIC RETICULUM DERIVED VESICLES.  
CC -1- MISCELLANEOUS: DELETION OF ERV14 PRODUCES DEFECTS IN YEAST CELL  
CC POLARITY. STRAINS HOMOLOGOUS FOR ERV14 DELETION DO NOT SPORULATE.  
CC -1- SIMILARITY: BELONGS TO THE CORNICION FAMILY.

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CC -----

CC EMBL; Z72576; CAA96756.1; -

CC PIR; S64058; S64058.

DR SGD; S0003022; ERV14.

DR GO; GO:0030138; C:COPII-coated vesicle; IDA.

DR GO; GO:0005789; C:endoplasmic reticulum membrane; IDA.

DR GO; GO:0007120; P:axial budding; IMP.

DR GO; GO:0006886; P:ER to Golgi transport; IMP.

DR GO; GO:0007151; P:sporulation (sensu Saccharomycetes); IMP.

DR InterPro; IPR003377; Cornichon.

DR Pfam; PF03311; Cornichon; 1.

DR PROSITE; PS01340; CORNICION; 1.

KW Endoplasmic reticulum; Transmembrane; Golgi stack.

FT INIT\_MET 0 0 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 1 5 POTENTIAL.

FT TRANSMEM 6 26 POTENTIAL.

FT DOMAIN 27 51 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 52 72 POTENTIAL.

FT DOMAIN 73 110 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 111 131 POTENTIAL.

FT DOMAIN 132 137 EXTRACELLULAR (POTENTIAL).

FT SEQUENCE 137 AA; 15799 MW; C90D4BDC2550CDC0 CRC64;

DR

Query Match 27.1%; Score 212.5; DB 1; Length 137;

```

DR   GeneDB SPombe: SPAC3C4.05; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM 8 28 POTENTIAL.
FT   TRANSMEM 54 74 POTENTIAL.
FT   TRANSMEM 113 133 POTENTIAL.
SQ   SEQUENCE 134 AA; 15738 MW; 71B58F624E87F523 CRC64;

Query Match      26.1%; Score 204.5; DB 1; Length 134;
Best Local Similarity 35.0%; Pred. No. 6e-13;
Matches 48; Conservative 30; Mismatches 52; Indels 7; Gaps 3;

QY   6 AAFVYMLALLTAALIFPAIHWHIAFDLKYDKNPIDOCNTLNPLVLPYLIHAFPCVM 65
DQ   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ   3 SAWIYFTSLMTLCANIMLQVFTVMYSDLKODFINPDLRSRLNWNVLPENMGFQAFSALL 62
QY   66 FLCAAEWLTGLNMPLLAYHWRVMSRPMVSGPLGYDPTTINNA-DI---LAYCKEGWCKLAF 125
DQ   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ   63 LLLSGAWITFLNVPMLAWN-----AKMNGNTHMDSTTIFPK-DVSSR-QKRSFFKLAC 115
QY   126 YLLAFFYYLYGMIVYLV 142
DQ   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ   116 FAVFFVYVLFVSVSLV 132

RESULT 11
YB60 YEAST
ID   YB60 YEAST STANDARD; PRT; 142 AA.
AC   P3812;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical 16.3 kDa protein in DUR1,2-AME1 intergenic region.
GN   YBR210W OR YBR1457.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C;
RA   Rieger M.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   -----
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CC   or send an email to license@isb-sib.ch)
CC   -----
DR   EMBL; Z36079; CAA85174.1; -.
DR   PIR; S46084; S46084.
DR   SGD; S0000414; YBR210W.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM 8 28 POTENTIAL.
FT   TRANSMEM 56 76 POTENTIAL.
FT   TRANSMEM 115 135 POTENTIAL.
SQ   SEQUENCE 142 AA; 16347 MW; E3329C122326A6A0 CRC64;

Query Match      24.7%; Score 193.5; DB 1; Length 142;
Best Local Similarity 32.4%; Pred. No. 7.3e-12;
Matches 45; Conservative 27; Mismatches 52; Indels 15; Gaps 3;

QY   10 YMLALLTAALIFPAIHWHIAFDLKYDKNPIDOCNTLNPLVLPYLIHAFPCVMFLCA 69

```

FT TRANSMEM 217 237 POTENTIAL.  
SQ SEQUENCE 256 AA; 28734 MW; F69971A264928DCC CRC64;  
  
Query Match 10.8%; Score 84.5; DB 1; Length 256;  
Best Local Similarity 22.2%; Pred. No. 0.37;  
Matches 32; Conservative 28; Mismatches 45; Indels 39; Gaps 7;  
  
QY 9 CYMLALLTAALIFPA--IWHIAFDLTKDYKNPIDQCNLTNPLVLPVLYLHFAFFCWMF 66  
DB 24 CVCVVLVEVALYFNSDIYHFA-----APLTAVMPKGMTATNIQTPTFTPIK 74  
QY 67 LCAAEWLTGLNPLLAYHWRMGRPMVSGPLVDP-----TTMNADILAYCQEGW 120  
DB 75 LTAI--VAIFISVPYLLYQIAFIA-----PALYQHEKRMYPILFSTLIFCYG----- 122  
QY 121 CKLAFVLLAFFYLYGMIVLVSS 144  
DB 123 -----VAFAYYI-----VPLVFS 136

Query Match 10.5%; Score 82.5; DB 1; Length 802;  
Best Local Similarity 21.8%; Pred. No. 1.8;  
Matches 29; Conservative 19; Mismatches 48; Indels 37; Gaps 5;  
  
QY 12 LALLTAALIFPAIWHIAFDLTKDYKNPIDQCNLTNPLVLPVLYLHFAFFCWMF 66  
DB 412 LFTLLSCGLMLAAWRTVFFARRSVALYN-----NPAALLYGDEVVLHXYGYTF 463  
QY 67 LCAAEWLTGLNPLLAYHWRMGRPMVSGPLVDP-----TTMNADILAYCQEGWCKLAPY 126  
DB 464 NANHYW-----WNIVLSY-----IFVKSLLVGFAAASQTQVLPM 499  
QY 127 LLAFFYLYGMIV 139  
DB 500 FILDFFVVAIIY 512

RESULT 14

ID NU4M CERCA STANDARD; PRT; 446 AA.  
AC Q34048; Q34053;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).  
GN ND4.  
OS Ceratitis capitata (Mediterranean fruit fly).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Tephritidae; Tephritidae; Ceratitis.  
OX NCBI\_TaxID=7213;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Guatemala laboratory colony, and Hawaii laboratory colony;  
RX MEDLINE=95261546; PubMed=7742977;  
RA Gasparich G.E., Sheppard W.S., Han H.Y., McPherson B.A., Steck G.J.;  
RT "Analysis of mitochondrial DNA and development of PCR-based  
RT diagnostic molecular markers for Mediterranean fruit fly (Ceratitis  
RT capitata) populations."  
RL Insect Mol. Biol. 4:61-67(1995).  
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
CC  
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CC  
CC ENBL; U12925; AAA85797.1; --  
DR ENBL; U12924; AAA85796.1; --  
DR InterPro; IPR003918; NADH\_oxred4.  
DR InterPro; IPR001750; Oxidored\_q1.  
DR InterPro; IPR000260; Oxidored\_q5\_N.  
DR Pfam; PF00361; oxidored\_q1; 1.  
DR Pfam; PF01059; oxidored\_q5\_N; 1.  
DR PRINTS; PR01437; NUOXDRD\_TASE4.  
DR KX Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
SQ SEQUENCE 446 AA; 50967 MW; E9AAAC06796897FD CRC64;

Query Match 10.3%; Score 81; DB 1; Length 446;  
Best Local Similarity 27.5%; Pred. No. 1.4;  
Matches 41; Conservative 21; Mismatches 35; Indels 52; Gaps 11;  
  
FT TRANSMEM 406 426 POTENTIAL.  
FT TRANSMEM 468 488 POTENTIAL.  
FT TRANSMEM 496 516 POTENTIAL.  
FT TRANSMEM 526 546 POTENTIAL.  
FT TRANSMEM 558 578 POTENTIAL.  
SQ SEQUENCE 802 AA; 90761 MW; 7BA13714AD912295 CRC64;  
  
Query Match 10.5%; Score 82.5; DB 1; Length 802;  
Best Local Similarity 21.8%; Pred. No. 1.8;  
Matches 29; Conservative 19; Mismatches 48; Indels 37; Gaps 5;  
  
QY 12 LALLTAALIFPAIWHIAFDLTKDYKNPIDQCNLTNPLVLPVLYLHFAFFCWMF 66  
DB 412 LFTLLSCGLMLAAWRTVFFARRSVALYN-----NPAALLYGDEVVLHXYGYTF 463  
QY 67 LCAAEWLTGLNPLLAYHWRMGRPMVSGPLVDP-----TTMNADILAYCQEGWCKLAPY 126  
DB 464 NANHYW-----WNIVLSY-----IFVKSLLVGFAAASQTQVLPM 499  
QY 127 LLAFFYLYGMIV 139  
DB 500 FILDFFVVAIIY 512

RESULT 13

ID YGN9\_YEAST STANDARD; PRT; 802 AA.  
AC PS3121;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 38, Last annotation update)  
DE Hypothetical 90.8 kDa protein in HUL5-SEC27 intergenic region.  
GN YGL139W OR G2812.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE OF 1-749 FROM N.A.  
RC STRAIN=S288c / FY1769;  
RX MEDLINE=9719798; PubMed=9046099;  
RA Voet M., Defoor E., Verhaesselt P., Riles L., Robben J., Volckaert G.;  
RT "The sequence of a nearly unclonable 22.8 kb segment on the left arm  
RT chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A,  
RT TPL, MRF1 genes and six new open reading frames."  
RL Yeast 13:177-182(1997).  
RN [2]  
RP SEQUENCE OF 616-802 FROM N.A.  
RC STRAIN=S288c / FY1679;  
RX Escaribano V., Erasó P., Portillo F., Mazon M.J.;  
RA "Sequence analysis of a 14.6 kb DNA fragment of Saccharomycetes  
RT cerevisiae chromosome VII reveals SEC27, SSM1b, a putative  
RT S-adenosylmethionine-dependent enzyme and six new open reading  
RT frames."  
RL Yeast 12:887-892(1996).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: TO YEAST YAL053W AND S.POMBE SPAC1F7.03.  
CC  
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CC  
CC ENBL; X99960; CAA68223.1; --  
DR ENBL; Z72661; CAA96851.1; --  
DR ENBL; Z72660; CAA96850.1; --  
DR ENBL; X92670; CAA63357.1; --  
DR PIR; S64153; S64153.  
DR SGD; S0003107; YGL139W.  
DR Hypothetical protein; Transmembrane.  
KW Hypothetical protein; 23 POTENTIAL.  
FT TRANSMEM 170 190 POTENTIAL.  
FT TRANSMEM 324 344 POTENTIAL.



QY 10 YMLALLTAAL-IPFAIWHIIAFDELKTDYKNPIDQCNTPINPLVLPYLIIHAFVCVMPIC 68  
 Db 142 YLLFTLVLSVPLLVGFIYLL-----YKN-----CNTMNFYLSNT-----MENC 180  
 QY 69 AAEMWLTGL-----NNPLLAYHIW-----RVMSRPVMSGPGLYDPTTIMNADILAYCKEGWC 121  
 Db 181 NLLYLAMILAFIVKMPFVLVHLPKHAVERPV-SG-----SMILAGIM-----L 224  
 QY 122 KLAFFV-LIAPFYLL-----YGMIVVLVS 143  
 Db 225 KLGYGGLAVFSLQLGLKYNIIWVSIS 253

## RESULT 15

P2L2\_MOUSE  
 ID P2L2\_MOUSE STANDARD; PRT; 621 AA.  
 AC Q9JLG4;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Polycystic kidney disease 2-like 2 protein (Polycystin-L2).  
 GN PKD2L2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=20221369; PubMed=10756092;  
 RA Guo L., Schreiber T.H., Weremowicz S., Morton C.C., Lee C., Zhou J.;  
 KT "Identification and characterization of a novel polycystin family  
 member, polycystin-L2, in mouse and human: sequence, expression,  
 alternative splicing, and chromosomal localization.";  
 RT Genomics 64:241-251(2000).  
 RL  
 CC -!- FUNCTION: May function as a subunit of a cation channel and play a  
 CU role in fertilization.  
 CC -!- TISSUE SPECIFICITY: Expressed only in testis and heart.  
 CC -!- SIMILARITY: BELONGS TO THE POLYCYSTIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AF182033; AAF65621.1; --  
 DR MGD; MGI:1858231; PKd2l2.  
 DR InterPro; IPR001682; Ca/Na\_pore.  
 DR InterPro; IPR002111; Cat channel\_TrpL.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR005820; M-channel\_nlg.  
 DR InterPro; IPR000434; PKD\_1.  
 DR InterPro; IPR003915; PKD\_2.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PR00500; POLYCYSTIN1.  
 DR PRINTS; PR01433; POLYCYSTIN2.  
 KW Ionic channel; Glycoprotein; Coiled coil; Transmembrane.  
 FT DOMAIN 1 31  
 FT TRANSMEM 32 52  
 FT DOMAIN 53 277  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 298  
 FT DOMAIN 299 314  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 315 335  
 FT DOMAIN 336 360  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 361 381  
 FT DOMAIN 382 406  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 407 427  
 FT DOMAIN 428 468  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 469 489  
 FT DOMAIN 490 621  
 FT CYTOPLASMIC (POTENTIAL).

FT SITE 126 138 POLYCYSTIN MOTIF.  
 FT DOMAIN 521 551 COILED COIL (POTENTIAL).  
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 621 AA; 73684 MW; 30430013DD6A7531 CRC64;  
 Query Match 10.1%; Score 79.5; DB 1; Length 621;  
 Best Local Similarity 17.9%; Pred. No. 2.7;  
 Matches 33; Conservative 31; Mismatches 51; Indels 69; Gaps 7;  
 QY 1 MAFTFAAFPCYMLALLTAALI-----FFAIWHI-----IA 30  
 Db 329 LAVSFYAYCNMQSFLLQLKNTDSYDPDFYFLAYWHIYYNNVIAITIFFPAWIKIFKIS 388  
 QY 31 FDELKTDYKNPIDQCNTPINPLVLPYLIIHAFVCVMPFLCAAEWLTGLMPLLAYHIWRYM 90  
 Db 389 FNETMSQLSSTLSRC--MKDIV-----GFAIMFFIIFSAYAQLGF-----426  
 QY 91 SRPVMSGPGLYDPTTIMNADI-----LAYCKEGCKLAFYLLAFYLYGYMIY 139  
 Db 427 ---LVFGSQVDDFSTFQNSIFAQFRIVLGDNFNFIQAQANWILGPYIFITFIFFVF---F 480  
 QY 140 VLVS 143  
 Db 481 VLLN 484  
 Search completed: September 11, 2003, 14:42:49  
 Job time : 30 secs



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OM protein - protein search, using sw model

Run on: September 11, 2003, 14:40:00 ; Search time 33 Seconds  
(without alignments)  
184.629 Million cell updates/sec

Title: US-09-918-585a-322  
Perfect score: 784  
Sequence: 1 MATFAFCVMLALLTAAL.....FYLLAFYYLYGMIVLVSS 144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgm2\_6/ptodata/1/iaa/5A-COMB.pep.\*
  - 2: /cgm2\_6/ptodata/1/iaa/5B-COMB.pep.\*
  - 3: /cgm2\_6/ptodata/1/iaa/6A-COMB.pep.\*
  - 4: /cgm2\_6/ptodata/1/iaa/6B-COMB.pep.\*
  - 5: /cgm2\_6/ptodata/1/iaa/PCTUS-COMB.pep.\*
  - 6: /cgm2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	784	100.0	144	2	US-08-950-168-1
2	784	100.0	144	4	US-09-365-705-1
3	784	100.0	144	4	US-09-702-705-327
4	784	100.0	144	4	US-09-736-457-327
5	784	100.0	145	4	US-09-257-179-63
6	548	69.9	144	2	US-08-950-168-3
7	548	69.9	144	4	US-09-365-705-3
8	244.5	31.2	139	4	US-09-489-847-219
9	244.5	31.2	155	4	US-09-489-847-374
10	196	25.0	35	4	US-09-257-179-120
11	173	22.1	30	4	US-09-257-179-119
12	167	21.3	30	4	US-09-257-179-118
13	84.5	10.8	163	3	US-09-053-197A-26
14	84.5	10.8	163	4	US-09-085-761A-26
15	84.5	10.8	2254	2	US-08-286-819A-28
16	84.5	10.8	2254	3	US-08-980-357-28
17	77.5	9.9	692	4	US-09-252-991A-23903
18	73.5	9.4	505	4	US-09-328-352-7155
19	72	9.2	251	4	US-09-191-468-72
20	72	9.2	251	4	US-09-191-468-74
21	72	9.2	251	4	US-09-191-468-76
22	72	9.2	251	4	US-09-191-468-78
23	72	9.2	251	4	US-09-191-468-80
24	72	9.2	251	4	US-09-191-468-82
25	72	9.2	251	4	US-09-191-468-84
26	72	9.2	251	4	US-09-191-468-86
27	72	9.2	797	2	US-08-700-013B-19

28	72	9.2	797	2	US-08-700-013B-21
29	72	9.2	797	3	US-09-182-728A-2
30	72	9.2	797	4	US-09-191-468-120
31	72	9.2	797	4	US-09-191-468-122
32	72	9.2	797	4	US-09-191-468-124
33	72	9.2	797	4	US-09-191-468-124
34	72	9.2	797	4	US-09-795-232-2
35	72	9.2	799	2	US-08-700-013B-27
36	71	9.1	578	4	US-09-740-041-4
37	70	8.9	177	2	US-08-700-013B-11
38	70	8.9	177	2	US-08-700-013B-13
39	69.5	8.9	307	4	US-09-393-634-19
40	69.5	8.9	307	4	US-09-393-634-53
41	68.5	8.7	526	4	US-09-205-815B-42
42	68	8.7	526	4	US-09-328-352-7475
43	67.5	8.6	542	1	US-08-246-583-3
44	67.5	8.6	542	1	US-09-636-791A-5
45	66.5	8.5	54	4	US-09-225-024-16

ALIGNMENTS

RESULT 1  
US-08-950-168-1  
; Sequence 1, Application US/08950168  
; Patent No. 5968744  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/950,168  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0401 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 144 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BLADNOT04  
; CLONE: 1318847  
; US-08-950-168-1

Query Match 100.0%; Score 784; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 3.8e-79;

*Wade*

	Matches	144;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MAFTFAACFYCMALLLTAALLI	FAIWHII	FADELKTDYKNP	IQDQNTNLPLV	PEYLIIHA	60			
Db	1	MAFTFAACFYCMALLLTAALLI	FAIWHII	FADELKTDYKNP	IQDQNTNLPLV	PEYLIIHA	60			
Qy	61	FFCWMFLCAAEWLTLGLNMP	LAYHII	WRVMSRPMVSGGLY	PTTIMNADII	LAYCQKEG	120			
Db	61	FFCWMFLCAAEWLTLGLNMP	LAYHII	WRVMSRPMVSGGLY	PTTIMNADII	LAYCQKEG	120			
Qy	121	CKLAFYLLAPFYLYGMIYV	LVS	144						
Db	121	CKLAFYLLAPFYLYGMIYV	LVS	144						

```

RESULT 2
US-09-365-705-1
; Sequence 1, Application US/09365705
; Patent No. 6348576
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Corley, Neil C.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

```

	Query Match	100.0%	Score 784;	DB 4;	Length 144;
	Best Local Similarity	100.0%;	Pred. No. 3.8e-79;		
	Matches 144;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAFTFAACYMLALLTAALIFFAIWHIIAFDELKTDYKNPFDQCNTLNPLVLPYLIHA	60		
Db	1	MAFTFAACYMLALLTAALIFFAIWHIIAFDELKTDYKNPFDQCNTLNPLVLPYLIHA	60		
Qy	61	FFCYMFLCAAEWLTLGNLPLLAYHIWYMSRPMWGPGLYDPTTIMNADILAYCOKG	120		

```

Db      61  PFCWFLCAEWLTLGLNMPJLAYHWRMSRPVMSGPCLYDPTTIMNADILAYCQKEG 120
QY      121 CKLAFYLLAFFYLYGMIYVLVSS 144
        |||||
Db      121 CKLAFYLLAFFYLYGMIYVLVSS 144
        |||||

RESULT 3
US-09-702-705-327
; Sequence/327/ Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-327

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	Query Match	100.0%;	Score 784;	DB 4;	Length 144;
	Best Local Similarity	100.0%;	Pred. No. 3.8e-79;		
	Matches 144;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps	0;
QY	1	MAETFAFCYMLALLTAALIFPAWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLIHA	60		
DDb	1	MAETFAFCYMLALLTAALIFPAWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLIHA	60		
QY	61	FFCWMFLCAAEWLTGLGNPLLAYHIIWRYMSRPVMSGPLGYDPTTIMNADILAYCQKSGW	120		
DDb	61	FFCWMFLCAAEWLTGLGNPLLAYHIIWRYMSRPVMSGPLGYDPTTIMNADILAYCQKSGW	120		
QY	121	CKLAFYLLAFFYYLYGMIYVLVSS	144		
DDb	121	CKLAFYLLAFFYYLYGMIYVLVSS	144		

RESULT 4  
US-09-736-457-327  
; Sequence 327, Application US/09736457  
; Patent No. 6509448  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; APPLICANT: Wang, Aijun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.478C15  
; CURRENT APPLICATION NUMBER: US/09/736,457  
; CURRENT FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 1864  
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-327

Query Match      100.0%; Score 784; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.8e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVLPYLIHA 60
Db 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVLPYLIHA 60

Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPLYDPTTINMADILAYCQKEGW 120
Db 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPLYDPTTINMADILAYCQKEGW 120

Qy 121 CKLAFYLLAFYYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFYYLYGMIYVLVSS 144

RESULT 5
US-09-257-179-63
; Sequence 63, Application US/09257179
; Patent No. 6410709
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 29 Human Secreted Proteins
; FILE REFERENCE: P2015P1
; CURRENT APPLICATION NUMBER: US/09/257,179
; CURRENT FILING DATE: 1999-02-25
; EARLIER APPLICATION NUMBER: PCT/US98/17709
; EARLIER FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 60/056,270
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,271
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,247
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,073
; EARLIER FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals stop translation
US-09-257-179-63

Query Match      100.0%; Score 784; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.8e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVLPYLIHA 60
Db 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVLPYLIHA 60

Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPLYDPTTINMADILAYCQKEGW 120
Db 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPLYDPTTINMADILAYCQKEGW 120

Qy 121 CKLAFYLLAFYYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFYYLYGMIYVLVSS 144

RESULT 6
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US-08-950-168-3
; Sequence 3, Application US/08950168
; Patent No. 5968744
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0401 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 886769
; US-08-950-168-3

Query Match      69.9%; Score 548; DB 2; Length 144;
Best Local Similarity 66.7%; Pred. No. 4.3e-53;
Matches 96; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVLPYLIHA 60
Db 1 MAFNFTAFTYVALIGDAGFLIFFAIHFVIAFDELKTDYKNPIDOCNSLNPLVLPYLIHI 60

Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPLYDPTTINMADILAYCQKEGW 120
Db 61 FLNLLFLFCGEWSLCINILIAHYIWRKNRPVMSGPLYDPTTVLKTDTLYRNMRGW 120

Qy 121 CKLAFYLLAFYYLYGMIYVLVSS 144
Db 121 IKLAVYLISFPYYIYGMVYSLIST 144

RESULT 7
US-09-365-705-3
; Sequence 3, Application US/09365705
; Patent No. 6348576
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Corley, Neil C.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
```

```

; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/365,705
; FILING DATE: 02-Aug-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: 14-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0401 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 886769
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-365-705-3

Query Match 69.9%; Score 548; DB 4; Length 144;
Best Local Similarity 66.7%; Pred. No. 4.3e-53;
Matches 96; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 MAFTFAFCYMLALLTAALIFPAIWHIIFAFDELKTDYKNPIDQCNTLNPLVLPYLIHA 60
Db 1 MAFTFAFYIYVALIGDAFLIFPAIWHIIFAFDELKTDYKNPIDQCNTLNPLVLPYLIHI 60

QY 61 FFCVMPFLCAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQEGW 120
Db 61 FLNLLFLFCGEWFLSCINIPLIAYHIWRYKRPVMSGPGLYDPTTLTKDITLYRNMGW 120

QY 121 CKLAFYLLAFFYLYGMIYVLVS 144
Db 121 IKLAVYLISFFYYIGMYSLIST 144

RESULT 8
US-09-489-847-219
; Sequence 219, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 374
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-374

Query Match 31.2%; Score 244.5; DB 4; Length 155;
Best Local Similarity 38.0%; Pred. No. 1.5e-19;
Matches 52; Conservative 24; Mismatches 60; Indels 1; Gaps 1;

QY 7 AFCYMLALLTAALIFPAIWHIIFAFDELKTDYKNPIDQCNTLNPLVLPYLIHAFPCVMF 66
Db 19 AVVFVSLDDCCALIFLSVFIITLSDLECDYINARSCCKLNKWKVIPELIGHTITVTYLL 78

QY 67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQEGWCKLAFY 126
Db 79 LMSLHWFIFLNLPAVTWNIYRIYINVP-SGNMGVDFDTEIHNRGOLKSHMKEMIKLGPH 137

QY 127 LLAFFYYLYGMIYVLVS 143
Db 127 LLAFFYYLYGMIYVLVS 143

RESULT 9
US-09-489-847-374
; Sequence 374, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 374
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-374

Query Match 31.2%; Score 244.5; DB 4; Length 155;
Best Local Similarity 38.0%; Pred. No. 1.5e-19;
Matches 52; Conservative 24; Mismatches 60; Indels 1; Gaps 1;

QY 7 AFCYMLALLTAALIFPAIWHIIFAFDELKTDYKNPIDQCNTLNPLVLPYLIHAFPCVMF 66
Db 19 AVVFVSLDDCCALIFLSVFIITLSDLECDYINARSCCKLNKWKVIPELIGHTITVTYLL 78

QY 67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQEGWCKLAFY 126
Db 79 LMSLHWFIFLNLPAVTWNIYRIYINVP-SGNMGVDFDTEIHNRGOLKSHMKEMIKLGPH 137

QY 127 LLAFFYYLYGMIYVLVS 143
Db 127 LLAFFYYLYGMIYVLVS 143

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Db 138 LLCFWLYSMILALIN 154

## RESULT 10

US-09-257-179-120  
; Sequence 120, Application US/09257179  
; Patent No. 6410709  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 29 Human Secreted Proteins  
; FILE REFERENCE: P2015P1  
; CURRENT APPLICATION NUMBER: US/09/257,179  
; EARLIER APPLICATION NUMBER: PCT/US98/17709  
; EARLIER FILING DATE: 1998-08-27  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 120  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-257-179-120

Query Match 25.0%; Score 196; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5.5e-15;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 WHIAFDELKTDYKNPIDQCNLTNPLVPEYLHA 60  
Db 1 WHIAFDELKTDYKNPIDQCNLTNPLVPEYLHA 35

## RESULT 11

US-09-257-179-119  
; Sequence 119, Application US/09257179  
; Patent No. 6410709  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 29 Human Secreted Proteins  
; FILE REFERENCE: P2015P1  
; CURRENT APPLICATION NUMBER: US/09/257,179  
; EARLIER APPLICATION NUMBER: PCT/US98/17709  
; EARLIER FILING DATE: 1998-08-27  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 119  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-257-179-119

Query Match 22.1%; Score 173; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHWRYM 90  
Db 1 FFCVMFLCAAEWLTGLNMPLLAYHWRYM 30

## RESULT 12

US-09-257-179-118  
; Sequence 118, Application US/09257179  
; Patent No. 6410709  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 29 Human Secreted Proteins  
; FILE REFERENCE: P2015P1  
; CURRENT APPLICATION NUMBER: US/09/257,179  
; EARLIER APPLICATION NUMBER: PCT/US98/17709  
; EARLIER FILING DATE: 1998-08-27  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 118  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-257-179-118

Query Match 21.3%; Score 167; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 7.3e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 SRPVMGPGLYDPTTMMNADILAYCQKEGW 120  
Db 1 SRPVMGPGLYDPTTMMNADILAYCQKEGW 30

## RESULT 13

US-09-053-197A-26  
; Sequence 26, Application US/09053197A  
; Patent No. 6022952  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Joel H.  
; APPLICANT: Turner, Raymond J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/053,197A  
; FILING DATE: 01-APR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Macknight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: UALB-03293  
; TELECOMMUNICATION INFORMATION:

	TELEPHONE:	(415) 705-8410	
	TELEFAX:	(415) 397-8338	
	INFORMATION FOR SEQ ID NO:	26:	
	SEQUENCE CHARACTERISTICS:		
	LENGTH:	163 amino acids	
	TYPE:	amino acid	
	STRANDEDNESS:	not relevant	
	TOPOLOGY:	unknown	
	MOLECULE TYPE:	protein	
	US-09-053-197A-26		
	Query Match	10.8%; Score 84.5; DB 3; Length 163;	
	Best Local Similarity	22.2%; Pred. No. 0.076;	
	Matches	32; Conservative 28; Mismatches 45; Indels 39; Gaps 7;	
QY	9	CYMLALLTLTAALIFPA--IWIIIAFDLTKDYKNPIDQCNTLNPLVLPEYLHAFPCVMF 66	
DB	14	CVICVVLVFVALVFNDSIYHFVA-----APLTAVMPKGTATNIQTPTFTPIK 64	
QY	67	LCAAEWLTLGLNPLLAIHYRYSRPVMSGPLYDP-----TTIMNADILAYCQKEGW 120	
DB	65	LTAI--VAIFISVPYLLYQIWAFTA-----PALYQHEKRMYPFLFSSTILFYCG---- 112	
QY	121	CKLAFVLLAFFYYLYGMIVLVSS 144	
DB	113	-----VAFAYI---VFPLVFS 126	
	RESULT 15		
	US-08-286-819A-28		
	; Sequence 28, Application US/08286819A		
	; Patent No. 5871910		
	; GENERAL INFORMATION:		
	; APPLICANT: ARTHUR, MICHEL		
	; APPLICANT: DUKTA-WALEN, SYLVIE		
	; APPLICANT: MOLINAS, CATHERINE		
	; APPLICANT: COURVALIN, PATRICE		
	; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE		
	; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPETIDES, IN PARTICULAR		
	; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR		
	; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS		
	; NUMBER OF SEQUENCES: 54		
	; CORRESPONDENCE ADDRESS:		
	; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,		
	; ADDRESSEE: P.C. Jefferson Davis Highway, Suite 400		
	; STREET: 1755 S. Arlington		
	; CITY: Arlington		
	; STATE: Virginia		
	; COUNTRY: U.S.A.		
	; ZIP: 22202		
	; COMPUTER READABLE FORM:		
	; MEDIUM TYPE: Floppy disk		
	; COMPUTER: IBM PC compatible		
	; OPERATING SYSTEM: PC-DOS/MS-DOS		
	; SOFTWARE: Patent In Release #1.0, Version #1.25		
	; CURRENT APPLICATION DATA:		
	; APPLICATION NUMBER: US/08/286,819A		
	; FILING DATE: 05-AUG-1994		
	; CLASSIFICATION: 435		
	; PRIOR APPLICATION DATA:		
	; APPLICATION NUMBER: US 08/174,682		
	; FILING DATE: 28-DEC-1993		
	; CLASSIFICATION: 435		
	; PRIOR APPLICATION DATA:		
	; APPLICATION NUMBER: US 07/917,146		
	; FILING DATE: 10-AUG-1992		
	; CLASSIFICATION: 435		
	; PRIOR APPLICATION DATA:		
	; APPLICATION NUMBER: PCT/FR/91/00855		
	; FILING DATE: 29-OCT-1991		
	; PRIOR APPLICATION DATA:		
	; APPLICATION NUMBER: FR 9013579		
	; FILING DATE: 31-OCT-1990		
	; CLASSIFICATION: 435		
	; ATTORNEY/AGENT INFORMATION:		
	; NAME: Oblon, No. 5871910man F.		
	; REGISTRATION NUMBER: 24,618		
	; REFERENCE/DOCKET NUMBER: 660-060-0 PCT		
	; TELECOMMUNICATION INFORMATION:		
	; TELEPHONE: (703) 413-3000		
	; TELEFAX: (703) 413-2220		
	; TELEX: 248855 OPAT UR		
	; INFORMATION FOR SEQ ID NO: 28:		
	; SEQUENCE CHARACTERISTICS:		
	; LENGTH: 2254 amino acids		
	; TYPE: amino acid		
	; TOPOLOGY: linear		
	US-09-085-761A-26		
	Query Match	10.8%; Score 84.5; DB 4; Length 163;	
	Best Local Similarity	22.2%; Pred. No. 0.076;	
	Matches	32; Conservative 28; Mismatches 45; Indels 39; Gaps 7;	
QY	9	CYMLALLTLTAALIFPA--IWIIIAFDLTKDYKNPIDQCNTLNPLVLPEYLHAFPCVMF 66	
DB	14	CVICVVLVFVALVFNDSIYHFVA-----APLTAVMPKGTATNIQTPTFTPIK 64	
QY	67	LCAAEWLTLGLNPLLAIHYRYSRPVMSGPLYDP-----TTIMNADILAYCQKEGW 120	
DB	65	LTAI--VAIFISVPYLLYQIWAFTA-----PALYQHEKRMYPFLFSSTILFYCG---- 112	
QY	121	CKLAFVLLAFFYYLYGMIVLVSS 144	
DB	113	-----VAFAYI---VFPLVFS 126	
	RESULT 14		
	US-09-085-761A-26		
	; Sequence 26, Application US/09085761A		
	; Patent No. 635178		
	; GENERAL INFORMATION:		
	; APPLICANT: Weiner, Joel H.		
	; APPLICANT: Turner, Raymond J.		
	; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN		
	; TITLE OF INVENTION: SECRETION		
	; NUMBER OF SEQUENCES: 77		
	; CORRESPONDENCE ADDRESS:		
	; ADDRESSEE: Medlen & Carroll, LLP		
	; STREET: 220 Montgomery Street, Suite 2200		
	; CITY: San Francisco		
	; STATE: California		
	; COUNTRY: United States of America		
	; ZIP: 94104		
	; COMPUTER READABLE FORM:		
	; MEDIUM TYPE: Floppy disk		
	; COMPUTER: IBM PC compatible		
	; OPERATING SYSTEM: PC-DOS/MS-DOS		
	; SOFTWARE: Patent In Release #1.0, Version #1.30		
	; CURRENT APPLICATION DATA:		
	; APPLICATION NUMBER: US/09/085,761A		
	; FILING DATE: 28-MAY-1998		
	; CLASSIFICATION: 435		
	; ATTORNEY/AGENT INFORMATION:		
	; NAME: Carroll, Peter G.		
	; REGISTRATION NUMBER: 32,837		
	; REFERENCE/DOCKET NUMBER: UALB-03356		
	; TELECOMMUNICATION INFORMATION:		
	; TELEPHONE: (415) 705-8410		
	; TELEF		



; MOLECULE TYPE: protein  
US-08-286-819A-28

Query Match 10.8%; Score 84.5; DB 2; Length 2254;  
Best Local Similarity 22.7%; Pred. No. 1.9;  
Matches 22; Conservative 16; Mismatches 32; Indels 27; Gaps 3;  
QY 50 PLVLPEYLI-----HAFPCWFLCAAEWLTGLNMPLLAYHIWRY----- 89  
Db 1114 PLASFFYLVPFTEVGLNVEHRYCL-----WMAGGRCTPCSFASLWRYGNDNRQVVG 1166  
QY 90 MSRPVMSGGLYDPTTINADILAYCOKEGWCKLAFY 126  
Db 1167 IQQIRAFQSMYQCGTIRDFLYSSCAEESRCEIYFY 1203

Search completed: September 11, 2003, 14:50:22  
Job time : 34 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:36:10 ; Search time 40 Seconds  
(without alignments)  
346.207 Million cell updates/sec

Title: US-09-918-585A-322  
Perfect score: 784  
Sequence: 1 MAFTFAAFCYMLALLLTAAL.....FYLLAFFYLYGMIYVLVSS 144

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	548	69.9	144	2 A56724	cni protein - frui
2	472	60.2	145	2 T24750	hypothetical prote
3	443	56.5	136	2 A9261	protein T0988.3 [i
4	212.5	27.1	138	2 S4058	probable membrane
5	204.5	26.1	134	2 T38516	cornichon homolog
6	193.5	24.7	142	2 S46084	probable membrane
7	159.5	20.3	126	2 D96653	hypothetical prote
8	128	16.3	160	2 G90096	hypothetical prote
9	128	16.3	160	2 H90129	hypothetical prote
10	128	16.3	160	2 B90133	hypothetical prote
11	122.5	15.6	145	2 T06616	hypothetical prote
12	90	11.5	249	2 T50162	hypothetical prote
13	86	11.0	259	2 AG0915	sec-independent pr
14	84.5	10.8	256	2 C64145	hypothetical prote
15	83.5	10.7	495	2 T20885	hypothetical prote
16	82.5	10.5	802	2 S64153	probable membrane
17	82	10.5	422	2 A83635	probable O-antigen
18	81	10.3	502	1 I30010	NADH2 dehydrogenas
19	81	10.3	502	2 T27908	hypothetical prote
20	79.5	10.1	2848	2 T32550	hypothetical prote
21	77.5	9.9	296	2 H69796	lactose permease h
22	77.5	9.9	661	2 G82985	probable choline t
23	77	9.8	270	2 F95978	probable sugar upt
24	77	9.8	270	2 C75473	probable Sec-indep
25	76.5	9.8	354	2 T22967	hypothetical prote
26	76.5	9.8	382	2 D58930	ubiquinol-cytochro
27	76	9.7	559	2 B72487	hypothetical prote
28	76	9.7	590	1 S34960	NADH2 dehydrogenas
29	75.5	9.6	209	1 S48459	probable dual spec

30	75.5	9.6	498	2 A97710	ADP,ATP carrier pr
31	75	9.6	484	2 T26190	hypothetical prote
32	74.5	9.5	292	2 AC1460	sugar ABC transpor
33	74.5	9.5	292	2 AD1097	sugar ABC transpor
34	74.5	9.5	323	2 F84526	hypothetical prote
35	74.5	9.5	458	2 S61974	SSU1 protein - yea
36	74	9.4	253	2 A83719	hypothetical prote
37	73	9.3	154	2 S30728	hypothetical prote
38	73	9.3	258	2 H65188	sec-independent pr
39	73	9.3	258	2 H91224	sec-independent pr
40	73	9.3	258	2 F86071	ubiquinol-cytochro
41	73	9.3	363	1 CSUTB	hypothetical prote
42	73	9.3	420	2 T32157	hypothetical prote
43	73	9.3	497	2 AG1768	hypothetical prote
44	73	9.3	1242	2 T39453	probable mrna stab
45	72.5	9.2	164	2 B81414	probable integral

ALIGNMENTS

RESULT 1

A56724

cni protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Jul-2000

C:Accession: A56724

R:Roth, S.; Neuman-Silberberg, F.S.; Barcelo, G.; Schuepbach, T.

Cell 81, 967-978, 1995

A:Title: cornichon and the EGF receptor signaling process are necessary for both anterior

A:Reference number: A56724; MUID:95300228; PMID:7540118

A:Accession: A56724

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-144 <ROT>

A:Cross-references: GB:U28069; NID:9886768; PIDN:AAA86527.1; PID:9886769

C:Genetics:

A:Gene: FlyBase:cni

A:Cross-references: FlyBase:FBgn0000339

C:Superfamily: Drosophila cornichon protein

Query Match 69.9%; Score 548; DB 2; Length 144;  
Best Local Similarity 66.7%; Pred. No. 9e-50;  
Matches 96; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLLTAALFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVLPYLIIHA 60

Db 1 MAFNFTAFYIYVIGDAFLIFFAIFHVIADFELKTDYKNPIDOCNSLNPLVLPYLIIHI 60

Qy 61 FFCVNFILCAAEWLTLGLNMLLAYHWRYSRPMVSGGLYDPTTMMADILAYCQKEGW 120

Db 61 FLNLLFLFCGEMFSLCINIPLIAVHWYKRWPMVSGGLYDPTTTLKLTLYRNMRSGW 120

Qy 121 CKLAPYLLAFYLYGMIYVLVSS 144

Db 121 IKLAVYLISFPYIYGMVYLSLT 144

RESULT 2

T24750

hypothetical protein T0988.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C:Accession: T24750

R:Steward, C.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19931

A:Accession: T24750

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-145 <WLL>

A:Cross-references: EMBL:Z78065; PIDN:CAB01516.2; GSPDB:GN00023; CESP:T09E8.3

A:Experimental source: Clone T09E8



```

Qy      70  AEWLTGLNNPLLAYHITWRYSRPMVSGPGLYDPTTMMNADILAYCQKEGWCKLAFYLLA 129
          | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db      67  GHWFMALLCPVLYYNFHLYSRK-----QHLIDVTEIFN--LLDWEKKKRLFKLAYIILT 119
          | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy     130  FFYYLY 135
          |
Db     120  LFLTIF 125
          | :

RESULT 8
G90096
hypothetical protein orf160 [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: G90096
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: G90096
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <DOU>
A:Cross-references: GB:AF165818; NID:g13794527; PIDN:AAK39902.1; GSPDB:GN00150
C:Genetics:
A:Gene: orf160
A:Map position: 1
A:Genome: nucleomorph
C:Keywords: nucleomorph

```

```

Query Match          16.3%; Score 128; DB 2; Length 160;
Best Local Similarity 29.4%; Pred. No. 4.9e-06;
Matches 32; Conservative 22; Mismatches 47; Indels 8; Gaps 3
33 ELKTDYKNPDDOQNTLNPVLPEYLIRAFCCVMFLCAAELTGLNMPLLAYHVIWYMSR 92
      :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db    38 DLSTDTVPNEVCCKNQKLKPEYLAHLFLSLAFVIRGWNIVGFLNFFPIYFNFAQW--- 94
      :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

Qy    93 PVMSGPGLYPTTTIMNADILAYCKQEGCKLAFYLLAFYYLYL-GMIVY 140
      :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db    95 --YEGKQLDSAQIFN--VLSRELRLVIKAKSAFFIIIVITWEMMIWV 139
      :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

RESULT 9
H90129
hypothetical protein orf160 [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H90129
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.;
Nature 410, 1091-1096, 2001
A>Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671

```

```

A;Accession: F90129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <DOU>
A;Cross-references: GB:AF083031; NID:gl3794404; PIDN:AAK39781.1; GSPDB:GN00152
C;Genetics:
A;Gene: orf160
A;Map position: 3
A;Genome: nucleomorph
C;Keywords: nucleomorph

Query Match      16.3%   Score 128; DB 2; Length 160;
Best Local Similarity 29.4%; Pred. No. 4.9e-06;
Matches 32; Conservative 22; Mismatches 47; Indels 8; Gaps 3

Oy          33 ELKTDYKNPDDQCNTPLPVLPEYLIIHAFCCWFLCAAEWLTLGLINMPLLAYHIWRYMSR 92
           :|||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

QY 93 PVMGPGGLYDPTTMMNADILAYCQKEGCKLAFYLLAFFYLY-GMIYV 140  
Db 95 --YEGKHQLDSAQIFN--VLSRELRTVIKSAFFIIIVITWEMWIV 139

RESULT 10  
B90133  
hypothetical protein orf160 [imported] - Guillardia theta nucleomorph  
C:Species: nucleomorph Guillardia theta  
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
C:Accession: B90133  
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reil  
Nature 410, 1091-1096, 2001  
A:Title: The highly reduced genome of an enslaved algal nucleus.  
A:Reference number: A99082; MUID:11323671; PMID:11323671  
A:Accession: B90133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-160 <DOU>  
A:Cross-references: GB:AF083031; NID:gl3794354; PIDN:AAK39731.1; GSPDB:GN00152  
C:Genetics:  
A:Gene: orf160  
A:Map position: 3  
A:Genome: nucleomorph  
C:Keywords: nucleomorph

Query Match 16.3%; Score 128; DB 2; Length 160;  
Best Local Similarity 29.4%; Pred. No. 4.9e-06;  
Matches 32; Conservative 22; Mismatches 47; Indels 8; Gaps 3;

QY 33 ELKTDYKNPIDQCNTLNPLVPEYLHAFPCVMFLCAAEWLTGLNMPLLAYHIWYMSR 92  
Db 38 DLSDTVNPVECDKVNQLKVPYLAHLFLSLAFVIRGVMWVIGFLNPFIFYNFAQW--- 94

QY 93 PVMGPGGLYDPTTMMNADILAYCQKEGCKLAFYLLAFFYLY-GMIYV 140  
Db 95 --YEGKHQLDSAQIFN--VLSRELRTVIKSAFFIIIVITWEMWIV 139

RESULT 11  
T06616  
hypothetical protein F16J13.160 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 22-Oct-1999  
C:Accession: T06616  
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,  
submitted to the Protein Sequence Database, April 1999  
A:Reference number: Z15789  
A:Accession: T06616  
A:Molecule type: DNA  
A:Residues: 1-145 <BEV>  
A:Cross-references: EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.160  
A:Experimental source: cultivar Columbia; BAC clone F16J13  
C:Genetics:  
A:Gene: AtSP:F16J13.160  
A:Map position: 4  
A:Introns: 34/3; 95/2; 136/2

Query Match 15.6%; Score 122.5; DB 2; Length 145;  
Best Local Similarity 29.0%; Pred. No. 1.7e-05;  
Matches 31; Conservative 21; Mismatches 48; Indels 7; Gaps 2;

QY 33 ELKTDYKNPIDQCNTLNPLVPEYLHAFPCVMFLCAAEWLTGLNMPLLAYHIWYMSR 92  
Db 40 DLEDFRINPDYSSRINRMVPEFGLQGLLYILTGHFWMAVLSPLFLYINIRLMYK 99

QY 93 PVMGPGGLYDPTTMMNADILAYCQKEGCKLAFYLLAFFYLY-GMIYV 139  
Db 100 -----EHLADVTLEYNTN--KWEQKRVYKIGHIALSIFITTYWLH 139

RESULT 12  
T50162  
hypothetical protein SPAC227.06 [imported] - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jun-2000  
C:Accession: T50162  
R:Zimmermann, W.; Wambutt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, November 1999  
A:Reference number: Z25036  
A:Accession: T50162  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-249 <ZIM>  
A:Cross-references: EMBL:AL133156; PIDN:CAB61455.1; GSPDB:GN00066; SPDB:SPAC227.06  
C:Experimental source: strain 972h(-); cosmid c227  
C:Genetics:  
A:Gene: SPDB:SPAC227.06  
A:Map position: 1

Query Match 11.5%; Score 90; DB 2; Length 249;  
Best Local Similarity 22.1%; Pred. No. 0.068;  
Matches 33; Conservative 26; Mismatches 50; Indels 40; Gaps 6;

QY 10 YMLALLTAALIFPA-----IWHIAFDELKTDYKNPIDQCNTLNPLVPEYLHAF 61  
Db 122 YSIKKLISAASIIYGYTTIIAVLLWGLVW-----NKNPKLLDCLCLYGY 167

QY 62 FCVMFLCAAEWLTGLNMP-----LLAYHIWYMSRPMVSGPLGYDPTTMMNADILAYC 115  
Db 168 AIV-----WLPVSLATPPFGLLSTLASHIVKY-----VLTGIGLLISIVFLTRNLYPIC 217

QY 116 QKEG--WCKLAFYLLAFFYLYGMIYV 142  
Db 218 QOAGSNLCKLLFGIIVFHCLLSLQLI 246

RESULT 13  
AG0915  
sec-independent protein translocase protein [imported] - Salmonella enterica subsp. ente  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AG0915  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AG0915  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-259 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD07917.1; PID:gl6504462; GSPDB:GN00176  
C:Genetics:  
A:Gene: tatC  
C:Superfamily: conserved hypothetical protein HI0188

Query Match 11.0%; Score 86; DB 2; Length 259;  
Best Local Similarity 23.7%; Pred. No. 0.19;  
Matches 33; Conservative 25; Mismatches 35; Indels 46; Gaps 8;

QY 9 CYMALLLTAALIFPA--IWHIAFDELK-----TDYKNPIDQCNTLNPLVPEY 56  
Db 23 CIVAVLLIFLALTYFANDYIHLVAAPLIKOMPGATMIATDVASPF-----TFPIKL--- 74

QY 57 LIHAFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPMVSGPLGYDPTTMMNADILAYCO 116  
Db 75 -----TFM-----VSLISAPVLYQWAFIA-----PALYKHERLLVVPPLVS--- 113

QY 117 KEGCKLAFYL-LAFFYLY 134

Db 114 ----SSLLFYIGWAFAYFV 128

RESULT 14

C64145

hypothetical protein HI0188 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Sep-1999

C:Accession: C64145

R: Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A: Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A. Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: C64145

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-256 <TIGR>

A:Cross-references: GB:U32704; GB:L42023; NID:g1573143; PIDN:AAC21857.1; PID:g1573146; T

A:Note: best homolog was a hypothetical protein from Escherichia coli

C:Superfamily: conserved hypothetical protein HI0188

Query Match 10.8%; Score 84.5; DB 2; Length 256;

Best Local Similarity 22.2%; Pred. No. 0.26;

Matches 32; Conservative 28; Mismatches 45; Indels 39; Gaps 7;

QY 9 CYMALALLTAALIFFA--IWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLLHAFFCVWF 66

Db 24 CVICVVLVFAVLYFSNDIYHFA-----APLTAVMPKGATMIATNIQTPEFTPIK 74

QY 67 LCAAEWLTLGLNPLLAYHIWYMRSPVMSGGLYDP-----TTMNADILAYCQEGW 120

Db 75 LTAL--VAIFISVPVLLQIWAFA-----PALYQHKRMIYPLLSSTILFYCG---- 122

QY 121 CKLAFYLLAFYLYGMIVLVSS 144

Db 123 -----VAFAYYI---VFPLVFS 136

RESULT 15

T20885

hypothetical protein F14D7.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T20885

R: Berks, M.

submitted to the EMBL Data Library, July 1996

A:Reference number: Z19340

A:Accession: T20885

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-495 <WIL>

A:Cross-references: EMBL:277658; PIDN:CAB01157.1; GSPDB:GN000023; CESP:F14D7.6

A:Experimental source: Clone F14D7

C:Genetics:

A:Gene: CESP:F14D7.6

A:Map position: 5

A:Introns: 20/1; 46/2; 90/3; 113/3; 142/1; 199/2; 218/2; 244/3; 301/1; 333/2; 451/2

Query Match 10.7%; Score 83.5; DB 2; Length 495;

Best Local Similarity 25.0%; Pred. No. 0.64;

Matches 41; Conservative 26; Mismatches 60; Indels 37; Gaps 11;

QY 3 FTFAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLLHAF 61

Db 265 FTVVAF--LMAIVCLAACVIVQCF-----FKENYVGIDKNSDSNVWIPKYDLAAL 315

QY 62 FCVMFLCAAE-----WLTGLNMPLLAYHIWYMRSP--VMSGGLYDPTTIM 107

Db 316 TCIVLFMIVNIATNVEVDKRIQMLIGLGFLL-YQVFWY----PWGFYSGPLDPLPDG-K 370

QY 108 NADILAYC-QKEGWCK-----LAFYLLAFYLYGMIVLVSS 144

Db 371 DTDVAGGCYQSYKWCQMTTRVPLPVYLLICFIVF-FGIAPFPVES 413

Search completed: September 11, 2003, 14:42:19

Job time : 47 secs





1	784	100.0	144	10	US-09-978-295A-322	Sequence 322, App
2	784	100.0	144	10	US-09-978-295A-322	Sequence 327, App
3	784	100.0	144	10	US-09-978-295A-322	Sequence 327, App
4	784	100.0	144	10	US-09-978-295A-322	Sequence 327, App
5	784	100.0	144	10	US-09-978-295A-322	Sequence 327, App
6	784	100.0	144	10	US-09-978-295A-322	Sequence 327, App
7	784	100.0	144	10	US-09-978-295A-322	Sequence 327, App
8	784	100.0	144	11	US-09-978-189-322	Sequence 322, App
9	784	100.0	144	11	US-09-978-189-322	Sequence 322, App
10	784	100.0	144	11	US-09-978-189-322	Sequence 322, App
11	784	100.0	144	11	US-09-978-189-322	Sequence 322, App
12	784	100.0	144	11	US-09-978-189-322	Sequence 322, App
13	784	100.0	144	11	US-09-978-189-322	Sequence 322, App
14	784	100.0	144	11	US-09-978-189-322	Sequence 322, App
15	784	100.0	144	11	US-09-978-189-322	Sequence 322, App

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[illegible]

us-09-918-585a-322.rapb

Tue Sep 16 17:51:16 2003

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;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 784; DB 10; Length 144;  
Best Local Similarity 100.0%; Pred. No. 2.9e-78;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

.Qy 1 MAFTFAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVLPYLIHA 60  
|||||  
Db 1 MAFTFAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVLPYLIHA 60  
|||||

Qy	61	FFCWFELCAAEWLTIGLNPLLAYHIWYNSRPFVMSGGLYDPTTINNADILAYCOKEGW	120
Db	61	FFCWFELCAAEWLTIGLNPLLAYHIWYNSRPFVMSGGLYDPTTINNADILAYCOKEGW	120
Qy	121	CKLAFYLLAFFYYLYGMIYVLVSS	144
Db	121	CKLAFYLLAFFYYLYGMIYVLVSS	144

## RESULT 4

US-09-902-941-327  
; Sequence 327, Application US/09902941  
; Patent No. US20020172952A1

; GENERAL INFORMATION:

APPLICANT: Henderson, Robert A.

; APPLICANT: Wang, Tongtong

APPLICANT: Watanabe. Yoshihi

**APPLICANT:** Johnson, Jeffrey

APPLICANT: Better, Marc W.

APPLICANT: Marnerakis Margarita  
 RECTOR, MAJOW.

APPLICANT: MATHEFAKIS, MARGA  
: CARTER DARRICK

APPLICANT: CARL, DARRICK  
: APPLICANT: FANGER, CARY D

APPLICANT: Fanger, Gary R.

APPLICANT: VEDVICK, Thomas S.

; APPLICANT: Bangur, Chaltanya

APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: AND DIAG

; FILE REFERENCE: 210121.478C17

; CURRENT APPLICATION NUMBER: US/0

; CURRENT FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 2002

; SOFTWARE: FastSEQ for Windows

; SEQ ID NO 327

LENGTH: 144

TYPE: PRT

ORGANISM: Homo

Query Match	100.0%	Score 784;	DB 10;
Best Local Similarity	100.0%	Pred. No. 2.9e-78;	Length 144;
Matches 144;	Conservative	0;	Mismatches 0;
			Indels 0;
			Gaps 0;

Qy	1	MAFTFAAFCCYMLALLLTAAALFFPAFWHIIA	AEDELKTDYKNPIDOCNTNLNLVLPEYLIHA	60
Db	1	MAFTFAAFCCYMLALLLTAAALFFPAFWHIIA	AEDELKTDYKNPIDOCNTNLNLVLPEYLIHA	60
Qy	61	FFCVMFLCAAEWLTLGLANPLLIAYHIWRYMSR	PVMSGGLYDPTTIINADILAYCOKEGW	120
Db	61	FFCVMFLCAAEWLTLGLANPLLIAYHIWRYMSR	PVMSGGLYDPTTIINADILAYCOKEGW	120

## RESULT 5

US-09-978-192A-322  
; Sequence 322, Application US/09978192A  
; Patent No. US20020177553A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi. Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton

APPLICANT: EALCON, DAN  
FERRARA NABOLSON

APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen

APPLICANT: FLIVAROFF, Ellen  
: FONG Sherman

APPLICANT: Fong, Sherman  
APPLICANT: Cao, Wei-Qing

APPLICANT: Gao, wei-Qiang

**APPLICANT:** Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E

APPLICANT: Goddard, Audrey

;; PRIOR APPLICATION NUMBER: 60/080194  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080327  
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Query Match 100.0%; Score 784; DB 10; Length 144;  
Best Local Similarity 100.0%; Pred. No. 2.9e-78; Mismatches 0; Indels 0; Gaps 0;  
Matches 144; Conservative 0;  
Qy 1 MAFTFAAFYMLALITLTAALIFFAIIHIAFDLKTQYKPNIDQCNLTNPLVLPYLIHA 60  
Db 1 MAFTFAAFYMLALITLTAALIFFAIIHIAFDLKTQYKPNIDQCNLTNPLVLPYLIHA 60  
Qy 61 PFCVMFLCAAEWLTGLNMLLAYHWRNRPVMSGPLYDPTTINMADILAYCQKEGW 120  
Db 61 PFCVMFLCAAEWLTGLNMLLAYHWRNRPVMSGPLYDPTTINMADILAYCQKEGW 120  
Qy 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
Db 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 6

US-09-999-832A-322  
; Sequence 322, Application US/09999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James,  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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; PRIOR APPLICATION NUMBER: 60/084414
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; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 784; DB 10; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 FFCVMFLCAAELWTLGLNMPLLAYHIWYMSRPMVSGPLYDPTTMMNADILAYCQKEGW 120
Db 61 FFCVMFLCAAELWTLGLNMPLLAYHIWYMSRPMVSGPLYDPTTMMNADILAYCQKEGW 120
Qy 121 CKLAFYLLAFFYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 8
US-09-978-189-322
; Sequence 322, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
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US-09-849-626-327
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-849-626-327

Query Match      100.0%; Score 784; DB 10; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 FFCVMFLCAAELWTLGLNMPLLAYHIWYMSRPMVSGPLYDPTTMMNADILAYCQKEGW 120
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Qy 121 CKLAFYLLAFFYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 7
US-09-849-626-327
; Sequence 327, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
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Qy 1 MAFTFAAFCYMLALLTLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVPEYLIHA 60
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Qy 61 FFCVMFLCAAELWTLGLNMPLLAYHIWYMSRPMVSGPLYDPTTMMNADILAYCQKEGW 120
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Qy 121 CKLAFYLLAFFYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFFYLYGMIYVLVSS 144
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3	PRIOR APPLICATION NUMBER: 60/076641	3	PRIOR FILING DATE: 1998-03-11
4	PRIOR APPLICATION NUMBER: 60/076649	4	PRIOR FILING DATE: 1998-03-11
5	PRIOR APPLICATION NUMBER: 60/077649	5	PRIOR FILING DATE: 1998-03-11
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17	PRIOR APPLICATION NUMBER: 60/079728	17	PRIOR FILING DATE: 1998-03-27
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25	PRIOR APPLICATION NUMBER: 60/080327	25	PRIOR FILING DATE: 1998-04-01
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19	PRIOR FILING DATE: 1998-04-27	
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21	PRIOR FILING DATE: 1998-04-28	
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43	PRIOR FILING DATE: 1998-05-05	
44	PRIOR APPLICATION NUMBER: 60/084414	
45	PRIOR FILING DATE: 1998-05-06	
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64	PRIOR APPLICATION NUMBER: 60/085323	
65	PRIOR FILING DATE: 1998-05-13	
66	PRIOR APPLICATION NUMBER: 60/085582	
67	PRIOR FILING DATE: 1998-05-15	
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69	PRIOR FILING DATE: 1998-05-15	
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match
Best Local Similarity 100.0%; Score 784; DB 11; Length 144;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120
Db 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120

Qy 121 CKLAFYLLAFFYLYGMIVLVSS 144
Db 121 CKLAFYLLAFFYLYGMIVLVSS 144

RESULT 9
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; Sequence 322, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrata, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 322
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-322

Query Match
Best Local Similarity 100.0%; Score 784; DB 11; Length 144;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIHA 60
Db 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIHA 60

Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120
Db 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120

Qy 121 CKLAFYLLAFFYLYGMIVLVSS 144
Db 121 CKLAFYLLAFFYLYGMIVLVSS 144

RESULT 9
US-09-978-608A-322
; Sequence 322, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrata, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 322
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-322

Query Match
Best Local Similarity 100.0%; Score 784; DB 11; Length 144;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIHA 60

Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120
Db 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120

Qy 121 CKLAFYLLAFFYLYGMIVLVSS 144
Db 121 CKLAFYLLAFFYLYGMIVLVSS 144

RESULT 9
US-09-978-585A-322
; Sequence 322, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrata, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 322
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-322

Query Match
Best Local Similarity 100.0%; Score 784; DB 11; Length 144;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIHA 60
Db 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIHA 60

Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120
Db 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120

Qy 121 CKLAFYLLAFFYLYGMIVLVSS 144
Db 121 CKLAFYLLAFFYLYGMIVLVSS 144

RESULT 10
US-09-978-585A-322
; Sequence 322, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrata, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 322
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-322

Query Match
Best Local Similarity 100.0%; Score 784; DB 11; Length 144;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIHA 60
Db 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIHA 60

Qy 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120
Db 61 FFCVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTMMNADILAYCOKEGW 120

Qy 121 CKLAFYLLAFFYLYGMIVLVSS 144
Db 121 CKLAFYLLAFFYLYGMIVLVSS 144
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Oy 121 CKLAFFYLLAFFYLYGMIVLVSS 144  
 Db 121 CKLAFFYLLAFFYLYGMIVLVSS 144

## RESULT 11

US-09-978-191A-322  
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 ; Publication No. US20030050239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
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 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C4  
 ; CURRENT APPLICATION NUMBER: US/09/978,191A  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
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56	PRIOR FILING DATE: 1998-05-15
57	PRIOR APPLICATION NUMBER: 60/085697

Qy	121	CKLAFYLLAFYYLYGMYIVLWSS	144
Db	121	CKLAFYLLAFYYLYGMYIVLWSS	144
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; Publication No. US20030050240A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi			
APPLICANT: Baker Kevin P.			
APPLICANT: Botstein, David			
APPLICANT: Deenoyers, Luc			
APPLICANT: Eaton, Dan			
APPLICANT: Ferrara, Napoleon			
APPLICANT: Filvaroff, Ellen			
APPLICANT: Fong, Sherman			
APPLICANT: Gao, Wei-Qiang			
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APPLICANT: Gerritsen, Mary E.			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
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APPLICANT: Gurney, Austin L.			
APPLICANT: Hillan, Kenneth J.			
APPLICANT: Kljavin, Ivar J.			
APPLICANT: Kuo, Sophia S.			
APPLICANT: Napier, Mary A.			
APPLICANT: Pan, James;			
APPLICANT: Paoni, Nicholas F.			
APPLICANT: Roy, Margaret Ann			
APPLICANT: Shelton, David L.			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumas, Daniel			
APPLICANT: Williams, P. Mickey			
APPLICANT: Wood, William I.			
TITLE OF INVENTION: Acids and Transmem			
TITLE OF INVENTION: Acids Encoding the			
FILE REFERENCE: P2630P1C17			
CURRENT APPLICATION NUMBER: US/09/978.4			
CURRENT FILING DATE: 2002-03-19			
PRIOR APPLICATION NUMBER: 09/918585			
PRIOR FILING DATE: 2001-07-30			
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 784; DB 11; Length 144;

Best Local Similarity 100.0%; Pred. No. 2.9e-78;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLYLHA 60

Db 1 MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLYLHA 60

Qy 61 FFCVNFCAAEWLTGLNMLLAYHIWYRSPVMSGFLYDPTTNADILAYCQKEGW 120

Db 61 FFCWFLCAAEWLTGLNPLLAYHWRVMSRPMVSGPLYDPTTMMNADILAYCQKEGW 120  
QY 121 CKLAFYLLAFFYLYGMIVLVSS 144  
Db 121 CKLAFYLLAFFYLYGMIVLVSS 144

RESULT 13  
US-09-978-564A-322  
; Sequence 322, Application US/09978564A  
; Publication No. US2003050241A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
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; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C25  
; CURRENT APPLICATION NUMBER: US/09/978,564A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918595  
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; PRIOR FILING DATE: 1998-05-15

Query Match      100.08; Score 784; DB 11; Length 144;
Best Local Similarity 100.08; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAFTFAAFYMLALLTLAALFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIIHA 60
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Qy 61 FFCVNFCAAEWLTGLNMLLAYHWRMSPVMSGPGLYDPTTMMNADILAYCQKEGW 120
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Db 61 FFCVNFCAAEWLTGLNMLLAYHWRMSPVMSGPGLYDPTTMMNADILAYCQKEGW 120
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; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C85
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
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Query Match 100.0%; Score 784; DB 11; Length 144;  
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Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVLPYLIHA 60



Qy 61 FFCVWFLCAEWLTLGLNPLLAHYHMYMSRPPVMSGGLYDPTTMMNADILAYCOKEGW 120  
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; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
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; APPLICANT: Kljavin, Ivar J.  
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; APPLICANT: Paoni, Nicholas F.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC12  
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13 PRIOR APPLICATION NUMBER: 60/083545  
14 PRIOR FILING DATE: 1998-04-29  
15 PRIOR APPLICATION NUMBER: 60/083554  
16 PRIOR FILING DATE: 1998-04-29  
17 PRIOR APPLICATION NUMBER: 60/083558  
18 PRIOR FILING DATE: 1998-04-29  
19 PRIOR APPLICATION NUMBER: 60/083559  
20 PRIOR FILING DATE: 1998-04-29  
21 PRIOR APPLICATION NUMBER: 60/083500  
22 PRIOR FILING DATE: 1998-04-29  
23 PRIOR APPLICATION NUMBER: 60/083742  
24 PRIOR FILING DATE: 1998-04-30  
25 PRIOR APPLICATION NUMBER: 60/084366  
26 PRIOR FILING DATE: 1998-05-05  
27 PRIOR APPLICATION NUMBER: 60/084414  
28 PRIOR FILING DATE: 1998-05-06  
29 PRIOR APPLICATION NUMBER: 60/084441  
30 PRIOR FILING DATE: 1998-05-06  
31 PRIOR APPLICATION NUMBER: 60/084637  
32 PRIOR FILING DATE: 1998-05-07  
33 PRIOR APPLICATION NUMBER: 60/084639  
34 PRIOR FILING DATE: 1998-05-07  
35 PRIOR APPLICATION NUMBER: 60/084640  
36 PRIOR FILING DATE: 1998-05-07  
37 PRIOR APPLICATION NUMBER: 60/084598  
38 PRIOR FILING DATE: 1998-05-07  
39 PRIOR APPLICATION NUMBER: 60/084600  
40 PRIOR FILING DATE: 1998-05-07  
41 PRIOR APPLICATION NUMBER: 60/084627  
42 PRIOR FILING DATE: 1998-05-07  
43 PRIOR APPLICATION NUMBER: 60/084643  
44 PRIOR FILING DATE: 1998-05-07  
45 PRIOR APPLICATION NUMBER: 60/085339  
46 PRIOR FILING DATE: 1998-05-13  
47 PRIOR APPLICATION NUMBER: 60/085338  
48 PRIOR FILING DATE: 1998-05-13  
49 PRIOR APPLICATION NUMBER: 60/085323  
50 PRIOR FILING DATE: 1998-05-13  
51 PRIOR APPLICATION NUMBER: 60/085582  
52 PRIOR FILING DATE: 1998-05-15  
53 PRIOR APPLICATION NUMBER: 60/085700  
54 PRIOR FILING DATE: 1998-05-15  
55 PRIOR APPLICATION NUMBER: 60/085689  
56 PRIOR FILING DATE: 1998-05-15  
57 PRIOR APPLICATION NUMBER: 60/085579  
58 PRIOR FILING DATE: 1998-05-15  
59 PRIOR APPLICATION NUMBER: 60/085580  
60 PRIOR FILING DATE: 1998-05-15  
61 PRIOR APPLICATION NUMBER: 60/085573  
62 PRIOR FILING DATE: 1998-05-15  
63 PRIOR APPLICATION NUMBER: 60/085704  
64 PRIOR FILING DATE: 1998-05-15  
65 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 784; DB 11; Length 144;  
Best Local Similarity 100.0%; Pred. No. 2.9e-78;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAFTFAFCYMLALLTALIFAIWHIIAFDELKTDYKNPIDQNTLNPLVLPYLIHA 60  
DB 1 MAFTFAFCYMLALLTALIFAIWHIIAFDELKTDYKNPIDQNTLNPLVLPYLIHA 60

QY 61 FFCVNFCAAEWLTGLNMPLLAYHIWYMSRPVMSGPLYDPTTIMNADILAYCQKGM 120  
DB 61 FFCVNFCAAEWLTGLNMPLLAYHIWYMSRPVMSGPLYDPTTIMNADILAYCQKGM 120  
QY 121 CKLAFYLLAFYFYLYGMIYVLVSS 144  
DB 121 CKLAFYLLAFYFYLYGMIYVLVSS 144

Search completed: September 11, 2003, 14:51:37  
Job time : 68 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:26:30 ; Search time 86 Seconds  
(without alignments)  
265.775 Million cell updates/sec

Title: US-09-918-585a-322

Perfect score: 784

Sequence: 1 MATFAFCYMLALLTAAL.....FYLLAFYYLYGMYIVLVSS 144

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*  
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2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
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10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	784	100.0	144	20	pk65_4 secreted protein
2	784	100.0	144	20	Human cornichon pr
3	784	100.0	144	20	Human PRO181 prote
4	784	100.0	144	20	Transmembrane doma
5	784	100.0	144	21	Human PRO181 (UNQ1
6	784	100.0	144	21	Antitumour PRO181
7	784	100.0	144	22	Human polypeptide,
8	784	100.0	144	22	Human lung tumour
9	784	100.0	144	23	Human cornichon pr

10	784	100.0	144	23	ABB95423	Human angiogenesis
11	784	100.0	144	23	AAE20143	Human cornichon pr
12	784	100.0	144	23	AAU85506	Clone #19110 of lu
13	784	100.0	144	23	ABB84817	Human PRO181 prote
14	784	100.0	144	23	AAU83651	Human PRO protein,
15	784	100.0	144	24	ABU69478	Human lung cancer
16	784	100.0	144	24	ABU66380	Lung cancer therap
17	784	100.0	144	24	ABU61118	Human PRO181 polyp
18	784	100.0	144	24	ABU07410	Protein differenti
19	784	100.0	145	20	AAV04316	Human secreted pro
20	775	98.9	142	21	AAV53622	A bone marrow secr
21	586	74.7	160	22	AA960454	Human cell cycle a
22	581	74.1	160	22	AA889196	Human secreted pro
23	575	73.3	160	23	ABB97539	Novel human protei
24	573	73.1	161	21	AAV76218	Human secreted pro
25	548	69.9	144	22	ABB61865	Drosophila melanog
26	548	69.9	144	22	ABB61866	Drosophila melanog
27	381	48.6	104	22	AAW41565	Human polypeptide
28	321	40.9	80	22	AAW39779	Human polypeptide
29	244.5	31.2	139	21	AAV91543	Human secreted pro
30	244.5	31.2	139	21	AAV78803	Hydrophobic domain
31	244.5	31.2	139	22	AAW79013	Human protein SEQ
32	244.5	31.2	139	22	AAW89173	Human secreted pro
33	244.5	31.2	139	23	AAW89737	Human polypeptide
34	244.5	31.2	139	24	ABR47720	Human secreted pro
35	244.5	31.2	149	22	ABB12002	Human secreted pro
36	244.5	31.2	149	22	AAW79997	Human protein SEQ
37	244.5	31.2	155	21	AAV91689	Human secreted pro
38	244.5	31.2	160	22	AAW25811	Human protein sequ
39	230	29.3	45	20	AAV11505	Human 5' EST secre
40	196	25.0	35	20	AAV04330	Fragment of human
41	186.5	23.8	157	22	ABB70572	Drosophila melanog
42	175.5	22.4	137	21	AAG16801	Arabidopsis thalia
43	173	22.1	30	20	AAV04329	Fragment of human
44	167	21.3	30	20	AAV04328	Fragment of human
45	164.5	21.0	146	21	AAG15261	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1  
AAV28813  
ID AAV28813 standard; Protein; 144 AA.  
XX  
AC AAV28813;  
XX  
DT 17-JAN-2000 (first entry)  
XX  
DE pk65\_4 secreted protein.  
XX  
KW clone pk65\_4; pk65\_4 protein; human foetal kidney cDNA library;  
KW secreted protein; Transmembrane domain; cytokine; tissue growth;  
KW TopPred II; computer program; COS cell expression system;  
KW membrane fraction; SDS polyacrylamide gel electrophoresis;  
KW nutritional activity; cell proliferation; immune stimulation;  
KW immune suppression; hematopoiesis regulation; tumour inhibition.  
XX  
OS Homo sapiens.  
XX  
PN W09950405-A1.  
XX  
PD 07-OCT-1999.  
XX  
PF 30-MAR-1999; 99WO-US06946.  
XX  
PR 31-MAR-1998; 98US-0080110.  
XX  
PA 29-MAR-1999; 99US-0280591.  
XX  
PI (GEMV ) GENETICS INST INC.  
XX  
PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ;





KW interaction assay; diagnosis; nutritional activity; cytokine;  
 KW cell proliferation; cell differentiation activity; immune stimulant;  
 KW immune suppressant; haematopoiesis regulator; tissue growth activity;  
 KW activin; inhibit activity; chemotaxis; chemokinesis; haemostasis;  
 KW thrombolysis; anti-inflammatory; cadherin; tumour invasion suppressor;  
 KW tumour inhibitor.

XX	Homo sapiens.
OS	
XX	WO9943802-A2.
PN	
XX	02-SEP-1999.
PD	
XX	
XX	25-FEB-1999; 99WO-JP00875.
PF	
XX	
XX	27-FEB-1998; 98JP-0046607.
XX	
XX	(PROT-) PROTEGENE INC.
PA	(SAGA ) SAGAMI CHEM RES. CENT.
PA	

AA	Sequence	144 AA;
SQ		

	Query Match	100.0%	Score 784;	DB 20;	Length 144;
	Best Local Similarity	100.0%;	Pred. No. 1.8e-85;		
	Matches 144;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAETFAAFCYMLALLTLTAALIFFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLIHA	60		
Db	1	MAETFAAFCYMLALLTLTAALIFFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLIHA	60		
Qy	61	FFCVMFCAAEWLTLGLNMPLLAHYIWRYSRPPVMSGFLYDPTTINMADILAYCQKEGW	120		
Db	61	FFCVMFCAAEWLTLGLNMPLLAHYIWRYSRPPVMSGFLYDPTTINMADILAYCQKEGW	120		
Qy	121	CKLAFYLLAFYYLYGMIYVLVSS	144		
Db	121	CKLAFYLLAFYYLYGMIYVLVSS	144		

RESULT 5  
AAB44288  
ID AAB44288 standard; Protein; 144 AA.  
XX  
XX AAB44288;  
XX  
XX 08-FEB-2001 (first entry)  
XX  
DT  
XX  
DE Human PRO181 (UNQ155) protein sequence SEQ ID NO:322.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Geritsen ME; Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kijavlin IJ, Kuo SS, Napier MA, Pan J, Pooni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WJ;

WPI; 2000-611443/58.  
N-PSDB: AAC78538.

Novel PRO polypeptides and polynucleotides used in detection methods to target bioactive molecules to specific cells, and to modulate cellular activities -

Claim 12; Fig 129; 636pp; English.

AACT8458 to AACT8599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AACT8987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.

AA	Sequence	144 AA;
SQ		

Query Match	Score 784;	DB 21;	Length 144;
100.0%			

	Best Local Similarity	100.0%;	Pred. No. 1.8e-85;	Mismatches	0;	Gaps	0;	
	Matches	14;	Conservative	0;	Indels	0;	Gaps	0;
Qy	1	MAFTFAAFCYMLALLLTAALFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLHA	60					
Db	1	MAFTFAAFCYMLALLLTAALFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPYLHA	60					
Qy	61	PFVCVMFLCAAEWLTLGLNMPLLAVHIWRYMSRPRVMSGPGLVDPTTIMNADILAYCQEGW	120					
Db	61	PFVCVMFLCAAEWLTLGLNMPLLAVHIWRYMSRPRVMSGPGLVDPTTIMNADILAYCQEGW	120					
Qy	121	CKLAFYLLAFFYLYGMIVLVSS	144					
Db	121	CKLAFYLLAFFYLYGMIVLVSS	144					

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RESULT 6
AAB19524
ID AAB19524 standard; Protein; 144 AA.
XX
XX AAB19524;
XX
XX 09-JAN-2001 (first entry)
XX
XX Antitumour PRO181 protein.
XX
XX PRO181; antitumour; antiproliferative; human; cancer; therapy;
XX drug screening.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX /label= Signal_peptide
XX FT FT
XX Domain 11..31
XX /label= Type-II_transmembrane_domain
XX FT FT
XX Domain 57..77
XX /label= Transmembrane_domain
XX FT FT
XX Domain 123..143
XX /label= Transmembrane_domain
XX Modified-site 96..100
XX /note= "Glycosaminoglycan attachment site"
XX
XX WO200053751-A1.
XX
XX
XX 14-SEP-2000.
XX
XX 30-DEC-1999; 99WO-US31243.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 28-MAR-1999; 99US-0126773.
XX 20-JUL-1999; 99US-0144758.
XX 08-SEP-1999; 99WO-US20594.
XX 20-DEC-1999; 99WO-US30999.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Napier MA, Wood WI;
XX WPI; 2000-594321/56.
XX N-PSDB; AAA88439.
XX
XX Novel PRO181 and PRO237 polypeptides useful for treating tumors
XX including cancers of breast, prostate, lung, leukemia in humans and for
XX identifying compounds capable of inhibiting growth of neoplastic cells
XX
XX Claim 19; Fig 2; 107pp; English.
XX
XX The present sequence is that of human PRO181 a novel inhibitor of
XX neoplastic cell growth. The sequence was deduced from a cDNA clone
XX (see AAA88439) isolated from a placental cDNA library. It shows
XX significant sequence similarity to cornichon protein. The

```

invention provides PRO181 and PRO237 (see AAB19525) polypeptides and polynucleotides, vectors, host cells, methods for their production, chimeric molecules and antibodies. Also claimed is a composition comprising PRO181 or PRO237, or their agonists, useful for the treatment of a tumour, especially breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, bladder cancer, central nervous system cancer, melanoma and leukaemia. PRO181 and PRO237 are also useful for treating neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, and blastocoelic disorders and inflammatory, angiogenic and immunologic disorders. They are useful for identifying agonists to PRO181 or PRO237 in drug screening and rational drug design.

```

Query Match          100.0%; Score 784; DB 21; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-95;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1  MATFFAAFCYMLALLTLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVLPYLIHA 60
Db      1  MATTFAAFCYMLALLTLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVLPYLIHA 60

QY      61  FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
Db      61  FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

QY      121  CKLAFYLLAFAFFLYLGYMIYVLVSS 144
Db      121  CKLAFYLLAFAFFLYLGYMIYVLVSS 144

RESULT 7
AAM93330
ID      AAM93330 standard; Protein; 144 AA.
XX
AC      AAM93330;
XX
DT      06-NOV-2001 (first entry)
XX
DE      Human polypeptide, SEQ ID NO: 2859.
XX
KW      Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS      Homo sapiens.
XX
PN      EPI130094-A2.
XX
PD      05-SEP-2001.
XX
PF      07-JUL-2000; 2000EP-0114089.
XX
PR      08-JUL-1999; 99JP-0194486.
PR      11-JAN-2000; 2000JP-0118774.
PR      02-MAY-2000; 2000JP-0183765.
XX
XX      (HELI-) HELIX RES INST.
XX
XX      Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX      WPI; 2001-524255/58.
DR      N-PSDB; AAK94250.
XX
XX      830 Primers useful for synthesizing full length cDNA clones and their
PT      use in genetic manipulation -
PT
XX
XX      Claim 8; SEQ ID NO 2859; 1380pp + sequence listing; English.
XX

CC      The invention relates to primers for synthesising full length cDNA
CC      clones. 830 cDNA molecules encoding a human protein have been
CC      isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA

```

CC molecules have been determined. Primers for synthesising the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones that were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a polypeptide  
 CC encoded by a full length human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 144 AA;  
 SQ Query Match 100.0%; Score 784; DB 22; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAFTFAAFYCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVPEYLIIHA 60  
 DB 1 MAFTFAAFYCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVPEYLIIHA 60  
 QY 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPGLYDPTTMMNADILAYCQKEGW 120  
 DB 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPGLYDPTTMMNADILAYCQKEGW 120  
 QY 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
 DB 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 8  
 AAB76851  
 ID AAB76851 standard; Protein; 144 AA.  
 XX AAB76851;  
 XX  
 DT 12-APR-2001 (first entry)  
 XX Human lung tumour protein related protein sequence SEQ ID NO:327.  
 DE Human; lung cancer; lung tumour; lung tumour protein; gene therapy;  
 XX lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;  
 KW cytostatic; antisense inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200100828-A2.  
 XX  
 XX 04-JAN-2001.  
 XX  
 XX 30-JUN-2000; 2000WO-US18061.  
 XX  
 XX 30-JUN-1999; 99US-0346492.  
 PR 15-OCT-1999; 99US-0419356.  
 PR 17-DEC-1999; 99US-0466867.  
 PR 30-DEC-1999; 99US-0476300.  
 PR 06-MAR-2000; 2000US-0519642.  
 PR 22-MAR-2000; 2000US-0533077.  
 PR 10-APR-2000; 2000US-0546259.  
 PR 27-APR-2000; 2000US-0560406.  
 PR 05-JUN-2000; 2000US-0589184.

XX (CORI-) CORIXA CORP.  
 XX  
 XX Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;  
 PI Retter MW, Mannion J;  
 XX WPI; 2001-071488/08.  
 XX Lung tumor-associated proteins and the nucleic acids that encode them,  
 PT useful for preventing, diagnosing and treating lung cancer -  
 XX Example 1; Page 254; 436pp; English.  
 XX

CC The present invention describes immunogenic portions of lung tumour-  
 CC associated proteins (I) and the nucleic acids (NAs) that encode them.  
 CC (I) have cytostatic activity and can be used in gene therapy, antisense  
 CC inhibition and in vaccines. The NAs and the lung tumour-associated  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with their inappropriate expression,  
 CC especially lung cancers. For example, the NAs may be administered to  
 CC treat diseases by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of the protein by expressing inactive proteins  
 CC or to supplement the patients own production of (I). Additionally, the  
 CC NAs may be used to produce the lung-tumour associated protein, according  
 CC to standard recombinant DNA methodology. Conversely, antisense NA  
 CC molecules may be administered to down regulate protein expression by  
 CC binding with the cells own genes and preventing their expression. The NA  
 CC and complementary sequences may also be used as DNA probes in diagnostic  
 CC assays to detect and quantitate the presence of similar NA sequences in  
 CC samples, and hence which patients may be in need of treatment for lung  
 CC cancer. The (I) may be used as antigens in the production of antibodies  
 CC and in assays to identify modulators (agonists and antagonists) of the  
 CC expression and activity of the protein. AAF68083 to AAF68878 and  
 CC AAB76848 to AAB76878 represent human lung tumour protein related  
 CC nucleotide and protein sequences which are used in the exemplification  
 CC of the present invention.

XX Sequence 144 AA;  
 SQ Query Match 100.0%; Score 784; DB 22; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAFTFAAFYCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVPEYLIIHA 60  
 DB 1 MAFTFAAFYCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVPEYLIIHA 60  
 QY 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPGLYDPTTMMNADILAYCQKEGW 120  
 DB 61 FFCVMFLCAAEWLTGLNMPLLAYHIWYMSRPVMSGPGLYDPTTMMNADILAYCQKEGW 120  
 QY 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
 DB 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 9  
 ABG31481  
 ID ABG31481 standard; Protein; 144 AA.  
 XX ABG31481;  
 XX  
 DT 20-NOV-2002 (first entry)  
 XX Human cornichon protein (CORN).  
 DE Human; cornichon protein; CORN; bladder cDNA library; BLADNOT04;  
 XX Incyte clone 1318847; developmental disorder; reproductive disorder;  
 KW immunological disorder; autoimmune disorder; neoplastic disorder;  
 KW microarray; cytostatic; antiinflammatory; gynaecological;  
 KW immunosuppressive.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002103342-A1.  
 XX  
 XX 01-AUG-2002.  
 XX  
 XX 10-JAN-2002; 2002US-0044477.  
 XX  
 XX 14-OCT-1997; 97US-0950168.  
 PR 02-AUG-1999; 99US-0365705.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX Hillman JL, Corley NC, Shah P;  
 PI



XX WPI: 2002-690628/74.  
 DR N-PSDB; ABK91098.  
 XX  
 PT New human cornichon protein and polynucleotide for diagnosing,  
 PT preventing or treating developmental, reproductive, immunological, and  
 PT neoplastic disorders -  
 XX  
 PS Claim 1; Fig 1; 32pp; English.  
 XX  
 CC The present invention relates to the isolation of human cornichon  
 CC protein (CORN), and the polynucleotide sequence encoding it. The  
 CC sequences are isolated from bladder cDNA library (SLADN0704) Incyte  
 CC clone 1318847. The polynucleotide and polypeptide sequences for  
 CC CORN are useful in the diagnosis, prevention, and treatment of  
 CC developmental disorders (e.g. anaemia, renal tubular acidosis,  
 CC Cushing's syndrome, dwarfism, epilepsy, hypothyroidism, glaucoma,  
 CC sensorineural hearing loss and cataract), reproductive disorders  
 CC (e.g. disorders of prolactin production, infertility, endometriosis,  
 CC polycystic ovary syndrome, endometrial and ovarian tumours, ectopic  
 CC pregnancy, prostate cancer, prostatitis, and carcinoma of the male  
 CC breast and gynaecomastia), immunological disorders (e.g. autoimmune  
 CC disorders, acquired immunodeficiency syndrome (AIDS), adult  
 CC respiratory distress syndrome, Addison's disease, allergies, anaemia,  
 CC asthma, atherosclerosis, gout, myocardial or pericardial inflammation,  
 CC osteoporosis, rheumatoid arthritis, scleroderma, systemic lupus  
 CC erythematosus, ulcerative colitis, haemodialysis, Crohn's disease,  
 CC atopic dermatitis, autoimmune thyroiditis, diabetes mellitus, Graves'  
 CC disease, glomerulonephritis, viral, bacterial, fungal, parasitic,  
 CC protozoal, helminthic infections and trauma), and neoplastic disorders  
 CC (e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, and various  
 CC cancers). CORN, fragments of CORN, and antibodies specific for CORN  
 CC are useful as elements on a microarray which is useful to monitor or  
 CC measure protein-protein interactions, drug-target interactions and  
 CC gene expression profiles. The present sequence represents human CORN.  
 XX  
 SQ Sequence 144 AA;  
 Query Match 100.0%; Score 784; DB 23; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAFTFAFCYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVLPYLIHA 60  
 DB 1 MAFTFAFCYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVLPYLIHA 60  
 QY 61 FFCVMFLCAEWLTGLNMPLLAYHIWYMRPVMSPGLYDPTTINMADILAYCQKEGW 120  
 DB 61 FFCVMFLCAEWLTGLNMPLLAYHIWYMRPVMSPGLYDPTTINMADILAYCQKEGW 120  
 QY 121 CKLAFYLLAFYYLYGMIYVLVSS 144  
 DB 121 CKLAFYLLAFYYLYGMIYVLVSS 144  
 RESULT 10  
 ID ABB95423  
 AC ABB95423 standard; Protein: 144 AA.  
 XX  
 AC ABB95423;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human angiogenesis related protein PRO181 SEQ ID NO: 2.  
 XX  
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW carotid; cycostatic; antiangiogenic; hypotensive; vulnary;  
 KW antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200208284-A2.

XX 31-JAN-2002.  
 PD 09-JUL-2001; 2001WO-US21735.  
 XX  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N P.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI: 2002-171999/22.  
 DR N-PSDB; ABL95561.  
 DR  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 11; Fig 2; 567pp; English.  
 XX

CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 144 AA;  
 SQ Query Match 100.0%; Score 784; DB 23; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAFTFAAFYCYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIIHA 60  
 DB 1 MAFTFAAFYCYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIIHA 60  
 QY 61 FFCVWFLCAAEWLTGLNPLLAYHWRVMSRPMVSGGLYDPTTINMADILAYCQKEGW 120  
 DB 61 FFCVWFLCAAEWLTGLNPLLAYHWRVMSRPMVSGGLYDPTTINMADILAYCQKEGW 120  
 QY 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
 DB 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 11  
 AAE20143  
 ID AAE20143 standard; Protein; 144 AA.  
 AC AAE20143;  
 DT 18-JUN-2002 (first entry)  
 DE Human cornichon protein (CORN).  
 XX Human; cornichon protein; CORN; Cushing's syndrome; muscular dystrophy;  
 KW developmental disorder; neoplastic; seizure; reproductive; immunological;  
 KW tubular acidosis; anaemia; polycystic ovary; autoimmune disorder; tumour;  
 KW breast cancer; prostate; testis; epilepsy; neuropathy; Addison's disease;  
 KW ulcerative colitis; spermatogenesis; hypothyroidism; cataract; arthritis;  
 KW infertility; galactorrhea; gynaeomastitis; diabetes mellitus; fungicide;  
 KW dermatitis; acquired immunodeficiency syndrome; AIDS; glomerulonephritis;  
 KW atherosclerosis; allergy; asthma; bronchitis; Crohn's disease; auditory;  
 KW gout; Graves' disease; multiple sclerosis; haemodialysis; anticonvulsant;  
 KW trauma; drug screening; ophthalmological; cytostatic; immunosuppressive;  
 KW gynaecological; antiulcer; nephrotropic; neuroprotective; antihelminthic;  
 KW antibacterial; tranquilizer; osteoporosis; antiparasitic; protozoacide;  
 KW vulnerary; virucide; gene therapy.

XX Homo sapiens.  
 XX US6348576-B1.  
 XX 19-FEB-2002.  
 XX 02-AUG-1999; 99US-0365705.  
 XX 14-OCT-1997; 97US-0950168.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Hillman JL, Corley NC, Shah P;  
 XX WPI; 2002-266544/31.  
 XX N-PSDB; AAD31079.

XX New human cornichon protein, useful for diagnosis, prevention and  
 XX treatment of developmental, reproductive, immunological and neoplastic  
 XX disorders and to screen for molecules that bind the protein

PS Claim 1; Fig 2; 29pp; English.

XX The invention relates to a purified human cornichon protein (CORN). CORN  
 CC is useful for diagnosis, prevention and treatment of developmental,  
 CC reproductive, immunological and neoplastic disorders. Developmental,  
 CC disorders include renal tubular acidosis, anaemia, Cushing's syndrome,  
 CC achondroplastic dwarfism, Duchenne and Becker muscular dystrophy,  
 CC epilepsy, hereditary neuropathies such as Charcot-Marie-Tooth disease,  
 CC neurofibromatosis, hypothyroidism, seizure disorders such as cerebral  
 CC palsy, cataract and sensorineural hearing loss and reproductive disorders  
 CC include disorders of prolactin production, infertility, ovulatory  
 CC defects, endometriosis, disruptions of the oestrous cycle, disruptions of  
 CC the menstrual cycle, polycystic ovary syndrome, endometrial and ovarian  
 CC tumours, autoimmune disorders, ectopic pregnancy, cancer of the breast,  
 CC galactorrhea, disruptions of spermatogenesis, cancer of the testis,  
 CC cancer of the prostate, prostatitis and carcinoma of the male breast and  
 CC gynaeomastitis. Immunological disorders include acquired immunodeficiency  
 CC syndrome (AIDS), diabetes mellitus, arthritis, including rheumatoid  
 CC arthritis, osteoarthritis, Addison's disease, allergic colitis, asthma,  
 CC atherosclerosis, bronchitis, Crohn's disease, ulcerative colitis, atopic  
 CC dermatitis, glomerulonephritis, gout, Graves' disease, multiple  
 CC sclerosis, osteoporosis, autoimmune thyroiditis, complications of cancer,  
 CC haemodialysis and extracorporeal circulation, viral bacterial, fungal,  
 CC parasitic, protozoal and helminthic infections, and trauma. CORN is  
 CC catalytic or immunogenic fragments is useful for screening libraries of  
 CC compounds in a variety of drug screening techniques. The present  
 CC sequence is human CORN. CORN gene is useful in gene therapy.

XX Sequence 144 AA;

Query Match 100.0%; Score 784; DB 23; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAFTFAAFYCYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIIHA 60  
 DB 1 MAFTFAAFYCYMLALLTAALFFAIWHIIAFDELKTDYKNPIDQCNLTNPLVPEYLIIHA 60  
 QY 61 FFCVWFLCAAEWLTGLNPLLAYHWRVMSRPMVSGGLYDPTTINMADILAYCQKEGW 120  
 DB 61 FFCVWFLCAAEWLTGLNPLLAYHWRVMSRPMVSGGLYDPTTINMADILAYCQKEGW 120  
 QY 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
 DB 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 12

AAU85506  
 ID AAU85506 standard; Protein; 144 AA.

XX AAU85506;  
 XX 21-MAY-2002 (first entry)  
 DT Clone #19110 of lung tumour protein.  
 DE Lung tumour; cancer; T cell; immune response stimulator;  
 XX cytostatic.  
 KW Homo sapiens.  
 OS WO200204514-A2.  
 XX 17-JAN-2002.  
 XX 10-JUL-2001; 2001WO-US22058.  
 XX 11-JUL-2000; 2000US-0614124.  
 XX 29-AUG-2000; 2000US-0651563.  
 XX 08-SEP-2000; 2000US-0658824.  
 XX 26-SEP-2000; 2000US-0671325.  
 XX 06-OCT-2000; 2000US-0677419.

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PR 30-OCT-2000; 2000US-0702705.
PR 13-DEC-2000; 2000US-0736457.
PR 03-MAY-2001; 2001US-0849626.
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
XX Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
XX McNabb A, Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
XX WPI; 2002-164634/21.
DR N-PSDB; ABK38061.
XX
XX Novel polynucleotide encoding a lung tumour polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumour protein
XX
XX Example 1; SEQ ID No 327; 223pp; English.
XX
XX The invention describes an isolated polynucleotide and polypeptide
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein for determining the presence of a cancer in a patient. A
CC composition containing the polynucleotide and/or polypeptide is useful
CC for treating a lung cancer in a patient. The polypeptide is useful for
CC removing tumour cells from a biological sample. The polynucleotide is
CC also useful as probe or primer to detect the level of mRNA encoding a
CC tumour protein. This is the amino acid sequence of a lung tumour
CC associated protein, described in the method of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 144 AA;
XX
XX Query Match 100.0%; Score 784; DB 23; Length 144;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-85;
XX Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MAFTFAAFVCMALLLTAALFFAIWHIIAFDELKTDYKNPIDQNTLNPLVPEYLHA 60
Db 1 MAFTFAAFVCMALLLTAALFFAIWHIIAFDELKTDYKNPIDQNTLNPLVPEYLHA 60
Qy 51 FFCVMFLCAEWLTLGLNMPLLAHYIWRYSRPMVSGPGLYDPTTINADILAYCQEGW 120
Db 61 FFCVMFLCAEWLTLGLNMPLLAHYIWRYSRPMVSGPGLYDPTTINADILAYCQEGW 120
Qy 121 CKLAFYLLAFYYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFYYLYGMIYVLVSS 144
XX
RESULT 13
ABB84817
ID ABB84817 standard; Protein; 144 AA.
XX
XX ABB84817;
XX
XX 16-MAY-2002 (first entry)
XX
XX Human PRO181 protein sequence SEQ ID NO:2.
XX
XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
XX vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping.
XX
XX Homo sapiens.
XX
XX WO200200690-A2.

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XX 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0665350.
XX 18-SEP-2000; 2000US-06654610.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 05-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001US-0866028.
XX 25-MAY-2001; 2001US-0866034.
XX 30-MAY-2001; 2001WO-US17092.
XX 30-MAY-2001; 2001US-0870574.
XX 01-JUN-2001; 2001WO-US17443.
XX 01-JUN-2001; 2001WO-US17800.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
XX N-PSDB; ABL88072.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 2; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX
XX Sequence 144 AA;

```

Query Match 100.0%; Score 784; DB 23; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFTFAAFYLLALLLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVPEYLIHA 60  
DB 1 MAFTFAAFYLLALLLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVPEYLIHA 60  
QY 61 FFCVWFLCAAELWLTGLNMPLLAYHIWYMSRPVMSGGLYDPTTINMADILAYCQKEGW 120  
DB 61 FFCVWFLCAAELWLTGLNMPLLAYHIWYMSRPVMSGGLYDPTTINMADILAYCQKEGW 120  
QY 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
DB 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 14  
AAU83651  
ID AAU83651 standard; Protein; 144 AA.  
XX AC AAU83651;  
XX DT 08-MAY-2002 (first entry)  
XX DE Human PRO protein, Seq ID No 120.  
XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
XX KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
XX KW pericyte cell proliferation; chondrocyte cell proliferation;  
XX KW tumour necrosis factor-alpha.  
XX OS Homo sapiens.  
XX SN WO200208288-A2.  
XX PD 31-JAN-2002.  
XX PF 29-JUN-2001; 2001WO-US21066.  
XX PR 20-JUL-2000; 2000US-219556P.  
XX PR 25-JUL-2000; 2000US-220585P.  
XX PR 25-JUL-2000; 2000US-220605P.  
XX PR 25-JUL-2000; 2000US-220607P.  
XX PR 25-JUL-2000; 2000US-220624P.  
XX PR 25-JUL-2000; 2000US-220636P.  
XX PR 25-JUL-2000; 2000US-220664P.  
XX PR 25-JUL-2000; 2000US-220666P.  
XX PR 26-JUL-2000; 2000US-220893P.  
XX PR 28-JUL-2000; 2000US-220710.  
XX PR 23-AUG-2000; 2000WO-US23522.  
XX PR 24-AUG-2000; 2000WO-US23328.  
XX PR 15-SEP-2000; 2000US-000000P.  
XX PR 10-NOV-2000; 2000WO-US30873.  
XX PR 28-NOV-2000; 2000US-253646P.  
XX PR 01-DEC-2000; 2000WO-US32678.  
XX PR 20-DEC-2000; 2000US-0747259.  
XX PR 20-DEC-2000; 2000WO-US34956.  
XX PR 28-FEB-2001; 2001WO-US06520.  
XX PR 10-MAY-2001; 2001US-0854280.  
XX PR 25-MAY-2001; 2001WO-US17092.  
XX PA (GETH ) GENENTECH INC.  
XX BK Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX WPI; 2002-172001/22.  
XX N-PSDB; ABK33595.  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal

PT tumour or liver tumour -  
XX Claim 11; Figure 120; 359pp; English.  
XX The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression in, pericyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
CC protein sequences of the invention.  
XX SQ Sequence 144 AA;  
Query Match 100.0%; Score 784; DB 23; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFTFAAFYLLALLLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVPEYLIHA 60  
DB 1 MAFTFAAFYLLALLLTAALIFFAIWHIIAFDELKTDYKNPIDOCNTLNPLVPEYLIHA 60  
QY 61 FFCVWFLCAAELWLTGLNMPLLAYHIWYMSRPVMSGGLYDPTTINMADILAYCQKEGW 120  
DB 61 FFCVWFLCAAELWLTGLNMPLLAYHIWYMSRPVMSGGLYDPTTINMADILAYCQKEGW 120  
QY 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
DB 121 CKLAFYLLAFFYLYGMIYVLVSS 144

RESULT 15  
ABU69478  
ID ABU69478 standard; Protein; 144 AA.  
XX AC ABU69478;  
XX DT 05-JUN-2003 (first entry)  
XX DE Human lung cancer associated cDNA #19110 protein.  
XX KW Human; lung cancer; lung tumour; cytostatic; vaccine;  
XX KW T cell expansion; CD4; CD8.  
XX OS Homo sapiens.  
XX SN US2002197669-A1.  
XX PD 26-DEC-2002.  
XX PF 03-MAY-2001; 2001US-0849626.  
XX PR 13-DEC-2000; 2000US-0736457.  
XX PA (BANG/) BANGUR C S.  
XX PA (FANG/) FANGER G R.  
XX PA (WANG/) WANG A.  
XX PA (WANG/) WANG T.  
XX PA (SWIT/) SWITZER A P.  
XX PA (MCNE/) MCNEILL P D.  
XX PA (CLAP/) CLAPPER J D.  
XX BK Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;  
PI Clapper JD;

Search completed: September 11, 2003, 14:41:26  
Job time : 88 secs

XX WPI: 2003-352750/33.  
DR N-PSDB; ACA10390.  
XX  
PT Novel lung cancer polynucleotide encoding lung cancer protein, useful  
PT for detecting the presence of lung cancer in a patient, and in  
PT pharmaceutical compositions, e.g. vaccines, for treating lung cancer -  
XX  
XX Example 1: Page -; 72pp: English.  
XX  
CC The invention relates to a polynucleotide encoding a lung tumour protein,  
CC comprising a sequence selected from any of the 14 sequences  
CC mentioned in the specification, or a sequence (S2) mentioned in  
CC specification, complement of S1, sequences consisting of at least 20  
CC contiguous residues of S1, sequences that hybridise to S1, sequences  
CC having 75%, preferably 90%, identity to S1, or degenerate variants of  
CC S1. Also included are an isolated polypeptide (comprising a sequence (S3)  
CC selected from any one of the 4 amino acid sequences mentioned in the  
CC specification, a sequence encoded by the polynucleotide, or sequences  
CC having at least 70%, preferably 90%, identity to a sequence encoded by  
CC the polynucleotide), an expression vector comprising the polynucleotide  
CC operably linked to an expression control sequence, a host cell  
CC transformed or transfected with the vector, an isolated antibody (or its  
CC antigen-binding fragment) that specifically binds to the polypeptide,  
CC detecting the presence of a cancer in a patient, a fusion protein  
CC comprising the polypeptide, an oligonucleotide that hybridises to  
CC S1 under moderately stringent conditions, stimulating and/or expanding T  
CC cells specific for a tumour protein (comprising contacting T cells with  
CC the polynucleotide, protein or antigen-presenting cells, under conditions  
CC and for a time sufficient to permit the stimulation and/or expansion of T  
CC cells) and inhibiting the development of a cancer in a patient (by  
CC incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with the  
CC polynucleotide, protein or antigen presenting cells that express the  
CC polynucleotide, such that T cells proliferate, administering to the  
CC patient an effective amount of the proliferated T cells, and thus  
CC inhibiting the development of a cancer in the patient. The  
CC polynucleotide, protein and cells are useful in a composition for  
CC stimulating an immune response in a patient, and for treating a cancer in  
CC a patient (particularly lung cancer). The oligonucleotide is useful for  
CC determining the presence of a cancer in a patient. The protein and  
CC oligonucleotides are useful in pharmaceutical compositions, e.g.  
CC vaccines. The polynucleotide is also useful as a probe or primer for  
CC nucleic acid hybridisation, and in the design and preparation of  
CC ribozyme molecules for inhibiting expression of tumour polypeptides and  
CC proteins in tumour cells. An amplified portion of the polynucleotide is  
CC useful for isolating a full-length gene from a suitable library.  
CC The present sequence is a protein encoded by a cDNA (full length,  
CC extended or partial) isolated from a library derived from lung tumour/  
CC cancer cells.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from the USPTO  
CC at seqdata.uspto.gov/sequence.html?DocId=20020197669.  
XX  
SQ Sequence 144 AA;  
Query Match 100.0%; Score 784; DB 24; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAFTFAAFCYMLALLTAALIFFAIIHIIAFDELKTDYKNPDCQNTLNPLVPEYLIHA 60  
Db 1 MAFTFAAFCYMLALLTAALIFFAIIHIIAFDELKTDYKNPDCQNTLNPLVPEYLIHA 60  
Qy 61 FFCVNFCAAEWLITGLNNPLLAYHIWRYMSRPVMSGPLDYDPTTMMNADILAYCQKEGW 120  
Db 61 FFCVNFCAAEWLITGLNNPLLAYHIWRYMSRPVMSGPLDYDPTTMMNADILAYCQKEGW 120  
Qy 121 CKLAFYLLAFFYLYGMIYVLVSS 144  
Db 121 CKLAFYLLAFFYLYGMIYVLVSS 144

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